

GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: February 13, 2006, 06:41:04 ; Search time 73 Seconds  
(without alignments)  
335.233 Million cell updates/sec

Title: US-10-601-311-1\_COPY\_143\_438

Perfect score: 1563

Sequence: 1 KTMNDFYLLKLGKTFCKV.....VPPFKQVTSYDTRFYDDEE 296

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Issued Patents AA:\*
- 1: /cgn2\_6/ptodata/1/1aa/5-COMB.pep.\*
  - 2: /cgn2\_6/ptodata/1/1aa/6-COMB.pep.\*
  - 3: /cgn2\_6/ptodata/1/1aa/H-COMB.pep.\*
  - 4: /cgn2\_6/ptodata/1/1aa/PCTUS-COMB.pep.\*
  - 5: /cgn2\_6/ptodata/1/1aa/RE-COMB.pep.\*
  - 6: /cgn2\_6/ptodata/1/1aa/backfilesl.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1563	100.0	465	2	US-09-526-043-2
2	1563	100.0	479	2	US-09-771-161A-246
3	1563	100.0	479	2	US-09-771-161A-247
4	1563	100.0	479	2	US-09-771-161A-248
5	1558	99.7	454	2	US-09-526-043-17
6	1394.5	89.2	480	2	US-09-590-740-6
7	1393.5	89.2	480	2	US-09-091-058-2
8	1393.5	89.2	480	2	US-09-590-740-2
9	1393.5	89.2	480	2	US-09-538-092-1053
10	1393.5	89.2	480	2	US-09-526-043-14
11	1393.5	89.2	480	2	US-09-771-161A-223
12	1393.5	89.2	726	2	US-09-417-197-71
13	1393.5	89.2	727	2	US-09-417-197-139
14	1391	89.0	480	2	US-09-526-043-13
15	1391	89.0	481	2	US-09-538-092-1054
16	1368.5	87.6	480	2	US-09-205-658-157
17	1364	87.3	417	2	US-09-590-740-4
18	1118.5	71.6	546	2	US-09-205-658-155
19	1107	70.8	352	2	US-09-771-161A-157
20	1098	70.2	541	2	US-09-205-658-154
21	1027	65.7	483	2	US-09-205-658-156
22	856	54.8	407	2	US-10-067-977-4
23	856	54.8	445	2	US-10-067-977-2
24	852	54.5	431	2	US-09-031-295-2
25	852	54.5	431	2	US-10-000-038-2
26	851.5	54.5	430	1	US-08-712-709-9
27	851.5	54.5	430	2	US-09-111-444-9

28	851.5	54.5	430	2	US-09-541-228-9	Sequence 9, Appli
29	848	54.3	431	1	US-08-712-709-5	Sequence 5, Appli
30	848	54.3	431	2	US-09-111-444-5	Sequence 5, Appli
31	848	54.3	431	2	US-09-541-228-5	Sequence 5, Appli
32	819.5	52.4	737	2	US-09-772-647-4	Sequence 4, Appli
33	819.5	52.4	737	2	US-10-228-931-4	Sequence 4, Appli
34	819.5	52.4	737	2	US-09-771-161A-195	Sequence 195, App
35	815	52.1	682	2	US-09-538-092-1003	Sequence 1003, Ap
36	815	52.1	739	2	US-09-949-016-7606	Sequence 7606, Ap
37	799.5	51.2	604	2	US-09-949-016-7547	Sequence 7547, Ap
38	790	50.5	671	6	5266464-2	Patent No. 5266464
39	779	49.8	673	2	US-09-538-092-853	Sequence 853, App
40	777	49.7	672	2	US-10-092-138A-27	Sequence 27, Appl
41	777	49.7	672	2	US-09-538-092-943	Sequence 943, App
42	777	49.7	672	2	US-08-681-219A-27	Sequence 27, Appl
43	771	49.3	916	2	US-09-417-197-73	Sequence 73, Appl
44	768.5	49.2	587	1	US-08-313-274-2	Sequence 2, Appli
45	768.5	49.2	655	2	US-09-949-016-11676	Sequence 11676, A

ALIGNMENTS

RESULT 1

US-09-526-043-2  
; Sequence 2, Application US/09526043  
; Patent No. 6881555  
; GENERAL INFORMATION:  
; APPLICANT: Guo, Kun  
; APPLICANT: Pagnoni, Marco  
; APPLICANT: Clark, Kenneth  
; APPLICANT: Ivashchenko, Yuri  
; TITLE OF INVENTION: AKT NUCLEIC ACIDS, POLYPEPTIDES, AND USES THEREOF  
; FILE REFERENCE: A3278A-US  
; CURRENT APPLICATION NUMBER: US/09/526,043  
; CURRENT FILING DATE: 2000-03-14  
; EARLIER APPLICATION NUMBER: 60/125,108  
; EARLIER FILING DATE: 1999-03-19  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 465  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-526-043-2

Query Match	100.0%	Score 1563;	DB 2;	Length 465;
Best Local Similarity	100.0%	Pred. No. 8.4e-141;	Mismatches 0;	Indels 0; Gaps 0;
Matches 296;	Conservative	0;		
Qy	1	KTMNDFYLLKLGKTFCKVILVREKASGKYAMKILKKEVIAKDEVAHTLTESRVLKN	60	
Db	143	KTMNDFYLLKLGKTFCKVILVREKASGKYAMKILKKEVIAKDEVAHTLTESRVLKN	202	
Qy	61	TRHPPLTSLKYSFQKDLRCFVMEYVNGGELFFHLSRVRVSEDTTRFYGABIVSALDYL	120	
Db	203	TRHPPLTSLKYSFQKDLRCFVMEYVNGGELFFHLSRVRVSEDTTRFYGABIVSALDYL	262	
Qy	121	HSGKIVYRDLKLENLMKDGHIKITDGLCKEGITDAATMTKTCGTPEYLAPEVLEND	180	
Db	263	HSGKIVYRDLKLENLMKDGHIKITDGLCKEGITDAATMTKTCGTPEYLAPEVLEND	322	
Qy	181	YGRAVDWNGLVGVVYEMMCGRLPFYVNOQHEKLFELIMEDIKFPRTLSDAKSLLSGLLI	240	
Db	323	YGRAVDWNGLVGVVYEMMCGRLPFYVNOQHEKLFELIMEDIKFPRTLSDAKSLLSGLLI	382	
Qy	241	KDPNKRLLGGGPDDAKEIMRHSFFSGVNWQDVYDKLVPPFKPQVTSYDTRFYDDEE	296	
Db	383	KDPNKRLLGGGPDDAKEIMRHSFFSGVNWQDVYDKLVPPFKPQVTSYDTRFYDDEE	438	

RESULT 2

US-09-771-161A-246

; Sequence 246, Application US/09771161A  
; Patent No. 6936450  
; GENERAL INFORMATION:  
; APPLICANT: LEVINE, et al.  
; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES  
; FILE REFERENCE: 802620-2005.1  
; CURRENT APPLICATION NUMBER: US/09/771.161A  
; CURRENT FILING DATE: 2001-01-26  
; PRIOR APPLICATION NUMBER: 09/724,676  
; PRIOR FILING DATE: 2000-11-28  
; PRIOR APPLICATION NUMBER: 136776  
; PRIOR FILING DATE: 2000-06-15  
; PRIOR APPLICATION NUMBER: 135619  
; PRIOR FILING DATE: 2000-04-12  
; NUMBER OF SEQ ID NOS: 273  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 245  
; LENGTH: 479  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-771-161A-246

Query Match 100.0%; Score 1563; DB 2; Length 479;  
Best Local Similarity 100.0%; Pred. No. 8.8e-141;  
Matches 296; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 KTMNDFYLLKLGKGTGKVLVREKASGKYAMKILKKEVIIAKDEVAHTLTESRVLKN 60  
Db 143 KTMNDFYLLKLGKGTGKVLVREKASGKYAMKILKKEVIIAKDEVAHTLTESRVLKN 202  
Qy 61 TRHPFLTSLKYSFQTKDRLCFVMEYVNGGELFFHLSRERVSEDRTRFYGAEIVSALDYL 120  
Db 203 TRHPFLTSLKYSFQTKDRLCFVMEYVNGGELFFHLSRERVSEDRTRFYGAEIVSALDYL 262  
Qy 121 HSGKIVYRDLKLENLMDKDGHIKITDGLCKEGITDAATMKTFCGTPPEYLAPEVLEDND 180  
Db 263 HSGKIVYRDLKLENLMDKDGHIKITDGLCKEGITDAATMKTFCGTPPEYLAPEVLEDND 322  
Qy 181 YGRAVDWVGLGVVMYEMMCGRLPFYNQDHEKLFELIIMEDIKFPRTLSSDAKSLLSGLLI 240  
Db 323 YGRAVDWVGLGVVMYEMMCGRLPFYNQDHEKLFELIIMEDIKFPRTLSSDAKSLLSGLLI 382  
Qy 241 KDPNKRLLGGGPDDAKEIMRHSFFSGVNWQVYDKLVPPFPKQVTSSETDTRYFDEE 296  
Db 383 KDPNKRLLGGGPDDAKEIMRHSFFSGVNWQVYDKLVPPFPKQVTSSETDTRYFDEE 438

RESULT 3  
US-09-771-161A-247  
; Sequence 247, Application US/09771161A  
; Patent No. 6936450  
; GENERAL INFORMATION:  
; APPLICANT: LEVINE, et al.  
; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES  
; FILE REFERENCE: 802620-2005.1  
; CURRENT APPLICATION NUMBER: US/09/771.161A  
; CURRENT FILING DATE: 2001-01-26  
; PRIOR APPLICATION NUMBER: 09/724,676  
; PRIOR FILING DATE: 2000-11-28  
; PRIOR APPLICATION NUMBER: 136776  
; PRIOR FILING DATE: 2000-06-15  
; PRIOR APPLICATION NUMBER: 135619  
; PRIOR FILING DATE: 2000-04-12  
; NUMBER OF SEQ ID NOS: 273  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 247  
; LENGTH: 479  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-771-161A-247

Query Match 100.0%; Score 1563; DB 2; Length 479;  
Best Local Similarity 100.0%; Pred. No. 8.8e-141;

Matches 296; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 KTMNDFYLLKLGKGTGKVLVREKASGKYAMKILKKEVIIAKDEVAHTLTESRVLKN 60  
Db 143 KTMNDFYLLKLGKGTGKVLVREKASGKYAMKILKKEVIIAKDEVAHTLTESRVLKN 202  
Qy 61 TRHPFLTSLKYSFQTKDRLCFVMEYVNGGELFFHLSRERVSEDRTRFYGAEIVSALDYL 120  
Db 203 TRHPFLTSLKYSFQTKDRLCFVMEYVNGGELFFHLSRERVSEDRTRFYGAEIVSALDYL 262  
Qy 121 HSGKIVYRDLKLENLMDKDGHIKITDGLCKEGITDAATMKTFCGTPPEYLAPEVLEDND 180  
Db 263 HSGKIVYRDLKLENLMDKDGHIKITDGLCKEGITDAATMKTFCGTPPEYLAPEVLEDND 322  
Qy 181 YGRAVDWVGLGVVMYEMMCGRLPFYNQDHEKLFELIIMEDIKFPRTLSSDAKSLLSGLLI 240  
Db 323 YGRAVDWVGLGVVMYEMMCGRLPFYNQDHEKLFELIIMEDIKFPRTLSSDAKSLLSGLLI 382  
Qy 241 KDPNKRLLGGGPDDAKEIMRHSFFSGVNWQVYDKLVPPFPKQVTSSETDTRYFDEE 296  
Db 383 KDPNKRLLGGGPDDAKEIMRHSFFSGVNWQVYDKLVPPFPKQVTSSETDTRYFDEE 438

RESULT 4  
US-09-771-161A-248  
; Sequence 248, Application US/09771161A  
; Patent No. 6936450  
; GENERAL INFORMATION:  
; APPLICANT: LEVINE, et al.  
; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES  
; FILE REFERENCE: 802620-2005.1  
; CURRENT APPLICATION NUMBER: US/09/771.161A  
; CURRENT FILING DATE: 2001-01-26  
; PRIOR APPLICATION NUMBER: 09/724,676  
; PRIOR FILING DATE: 2000-11-28  
; PRIOR APPLICATION NUMBER: 136776  
; PRIOR FILING DATE: 2000-06-15  
; PRIOR APPLICATION NUMBER: 135619  
; PRIOR FILING DATE: 2000-04-12  
; NUMBER OF SEQ ID NOS: 273  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 248  
; LENGTH: 479  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-771-161A-248

Query Match 100.0%; Score 1563; DB 2; Length 479;  
Best Local Similarity 100.0%; Pred. No. 8.8e-141;  
Matches 296; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 KTMNDFYLLKLGKGTGKVLVREKASGKYAMKILKKEVIIAKDEVAHTLTESRVLKN 60  
Db 143 KTMNDFYLLKLGKGTGKVLVREKASGKYAMKILKKEVIIAKDEVAHTLTESRVLKN 202  
Qy 61 TRHPFLTSLKYSFQTKDRLCFVMEYVNGGELFFHLSRERVSEDRTRFYGAEIVSALDYL 120  
Db 203 TRHPFLTSLKYSFQTKDRLCFVMEYVNGGELFFHLSRERVSEDRTRFYGAEIVSALDYL 262  
Qy 121 HSGKIVYRDLKLENLMDKDGHIKITDGLCKEGITDAATMKTFCGTPPEYLAPEVLEDND 180  
Db 263 HSGKIVYRDLKLENLMDKDGHIKITDGLCKEGITDAATMKTFCGTPPEYLAPEVLEDND 322  
Qy 181 YGRAVDWVGLGVVMYEMMCGRLPFYNQDHEKLFELIIMEDIKFPRTLSSDAKSLLSGLLI 240  
Db 323 YGRAVDWVGLGVVMYEMMCGRLPFYNQDHEKLFELIIMEDIKFPRTLSSDAKSLLSGLLI 382  
Qy 241 KDPNKRLLGGGPDDAKEIMRHSFFSGVNWQVYDKLVPPFPKQVTSSETDTRYFDEE 296  
Db 383 KDPNKRLLGGGPDDAKEIMRHSFFSGVNWQVYDKLVPPFPKQVTSSETDTRYFDEE 438

RESULT 5

US-09-526-043-17  
; Sequence 17, Application US/09526043  
; Patent No. 6681555  
; GENERAL INFORMATION:  
; APPLICANT: Guo, Kun  
; APPLICANT: Pagnoni, Marco  
; APPLICANT: Clark, Kenneth  
; APPLICANT: Ivaschenko, Yuri  
; TITLE OF INVENTION: AKT NUCLEIC ACIDS, POLYPEPTIDES, AND USES THEREOF  
; FILE REFERENCE: A3278A-US  
; CURRENT APPLICATION NUMBER: US/09/526,043  
; CURRENT FILING DATE: 2000-03-14  
; EARLIER APPLICATION NUMBER: 60/125,108  
; EARLIER FILING DATE: 1999-03-19  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 17  
; LENGTH: 454  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: PCR Primer  
US-09-526-043-17

Query Match 99.7%; Score 1558; DB 2; Length 454;  
Best Local Similarity 99.7%; Pred. No. 2.5e-140;  
Matches 295; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KTMNDFYLLKLGKGTGKVIIVREKASGYAMKILKEVIAKDEVAHTLTESRVLKN 60  
DB 143 KTMNDFYLLKLGKGTGKVIIVREKASGYAMKILKEVIAKDEVAHTLTESRVLKN 202  
QY 61 TRHPFLTSKYSFQTKDRLCFVMEYVNGGELFFHLSRERVSFSDRTRFYGAIVSALDYL 120  
DB 203 TRHPFLTSKYSFQTKDRLCFVMEYVNGGELFFHLSRERVSFSDRTRFYGAIVSALDYL 262  
QY 121 HSGKIVYRDLEKLEMLDKGHIKITDGLCKEGITDAATMTKTCGTPEYLAPEVLEND 180  
DB 263 HSGKIVYRDLEKLEMLDKGHIKITDGLCKEGITDAATMTKTCGTPEYLAPEVLEND 322  
QY 181 YGRAVDWGLGVVYEMMCGRLPFYNQDHEKLFELILMEDIKFPRTLSSDAKSLGLLI 240  
DB 323 YGRAVDWGLGVVYEMMCGRLPFYNQDHEKLFELILMEDIKFPRTLSSDAKSLGLLI 382

QY 241 KDPNKRLLGGGPDDAKEIMRHSFFSGVNMQDVYDKLVPPFKPQVTSSETDTRYFDEE 296  
DB 383 KDPNKRLLGGGPDDAKEIMRHSFFSGVNMQDVYDKLVPPFKPQVTSSETDTRYFDEE 438

RESULT 6  
US-09-590-740-6  
; Sequence 6, Application US/09590740  
; Patent No. 6689807  
; GENERAL INFORMATION:  
; APPLICANT: Kenneth Walsh  
; APPLICANT: St. Elizabeth's Medical Center  
; TITLE OF INVENTION: HMG CoA Reductase Inhibitors for  
; TITLE OF INVENTION: Promoting Angiogenesis  
; FILE REFERENCE: 49,784 (1417)  
; CURRENT APPLICATION NUMBER: US/09/590,740  
; CURRENT FILING DATE: 2000-06-08  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 6  
; LENGTH: 480  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-590-740-6

Query Match 89.2%; Score 1394.5; DB 2; Length 480;  
Best Local Similarity 87.8%; Pred. No. 1.1e-124;  
Matches 260; Conservative 20; Mismatches 15; Indels 1; Gaps 1;

QY 2 TMDNDFYLLKLGKGTGKVIIVREKASGYAMKILKEVIAKDEVAHTLTESRVLKN 61  
DB 146 TMDNDFYLLKLGKGTGKVIIVREKATGRYYAMKILKEVIAKDEVAHTLTENRVLQNS 205  
QY 62 RHPFLTSKYSFQTKDRLCFVMEYVNGGELFFHLSRERVSFSDRTRFYGAIVSALDYL 121  
DB 206 RHPFLTSKYSFQTKDRLCFVMEYVNGGELFFHLSRERVSFSDRTRFYGAIVSALDYL 265  
QY 122 SGK-IVYRDLEKLEMLDKGHIKITDGLCKEGITDAATMTKTCGTPEYLAPEVLEND 180  
DB 266 SGKVVYRDLEKLEMLDKGHIKITDGLCKEGIKDGTATMTKTCGTPEYLAPEVLEND 325  
QY 181 YGRAVDWGLGVVYEMMCGRLPFYNQDHEKLFELILMEDIKFPRTLSSDAKSLGLLI 240  
DB 326 YGRAVDWGLGVVYEMMCGRLPFYNQDHEKLFELILMEDIKFPRTLSSDAKSLGLLI 385  
QY 241 KDPNKRLLGGGPDDAKEIMRHSFFSGVNMQDVYDKLVPPFKPQVTSSETDTRYFDEE 296  
DB 386 KDPNKRLLGGGPDDAKEIMRHSFFSGVNMQDVYDKLVPPFKPQVTSSETDTRYFDEE 441

RESULT 7  
US-09-091-058-2  
; Sequence 2, Application US/09091058  
; Patent No. 6054285  
; GENERAL INFORMATION:  
; APPLICANT: Hemmings, Brian A.  
; APPLICANT: Frech, Matthias  
; TITLE OF INVENTION: Screening Method  
; FILE REFERENCE: 4-20683/A/20684/PCT  
; CURRENT APPLICATION NUMBER: US/09/091,058  
; CURRENT FILING DATE: 1998-06-10  
; EARLIER APPLICATION NUMBER: PCT/EP96/04814  
; EARLIER FILING DATE: 1996-11-05  
; EARLIER APPLICATION NUMBER: 9525703.6  
; EARLIER FILING DATE: 1995-12-15  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: Patent In Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 480  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-091-058-2

Query Match 89.2%; Score 1393.5; DB 2; Length 480;  
Best Local Similarity 87.8%; Pred. No. 1.3e-124;  
Matches 260; Conservative 20; Mismatches 15; Indels 1; Gaps 1;

QY 2 TMDNDFYLLKLGKGTGKVIIVREKASGYAMKILKEVIAKDEVAHTLTESRVLKN 61  
DB 146 TMDNDFYLLKLGKGTGKVIIVREKATGRYYAMKILKEVIAKDEVAHTLTENRVLQNS 205  
QY 62 RHPFLTSKYSFQTKDRLCFVMEYVNGGELFFHLSRERVSFSDRTRFYGAIVSALDYL 121  
DB 206 RHPFLTSKYSFQTKDRLCFVMEYVNGGELFFHLSRERVSFSDRTRFYGAIVSALDYL 265  
QY 122 SGK-IVYRDLEKLEMLDKGHIKITDGLCKEGITDAATMTKTCGTPEYLAPEVLEND 180  
DB 266 SGKVVYRDLEKLEMLDKGHIKITDGLCKEGIKDGTATMTKTCGTPEYLAPEVLEND 325  
QY 181 YGRAVDWGLGVVYEMMCGRLPFYNQDHEKLFELILMEDIKFPRTLSSDAKSLGLLI 240  
DB 326 YGRAVDWGLGVVYEMMCGRLPFYNQDHEKLFELILMEDIKFPRTLSSDAKSLGLLI 385  
QY 241 KDPNKRLLGGGPDDAKEIMRHSFFSGVNMQDVYDKLVPPFKPQVTSSETDTRYFDEE 296  
DB 386 KDPNKRLLGGGPDDAKEIMRHSFFSGVNMQDVYDKLVPPFKPQVTSSETDTRYFDEE 441

RESULT 8  
US-09-590-740-2  
; Sequence 2, Application US/09590740  
; Patent No. 6689807

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; GENERAL INFORMATION:
; APPLICANT: Kenneth Walsh
; APPLICANT: St. Elizabeth's Medical Center
; TITLE OF INVENTION: HMG CoA Reductase Inhibitors for
; TITLE OF INVENTION: Promoting Angiogenesis
; FILE REFERENCE: 49,784 (1417)
; CURRENT APPLICATION NUMBER: US/09/590,740
; CURRENT FILING DATE: 2000-06-08
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 480
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-590-740-2

Query Match      89.2%; Score 1393.5; DB 2; Length 480;
Best Local Similarity 87.8%; Pred. No. 1.3e-124;
Matches 260; Conservative 20; Mismatches 15; Indels 1; Gaps 1;

Qy  2  TMNDFYLLKLGKGTGKVLVREKASGKYAMKILKKEVIAKDEVAHTLTESRVLKNT 61
Db  146  TMNEFEYLKLGKGTGKVLVREKATGRYYAMKILKKEVIAKDEVAHTLTENRVLQNS 205

Qy  62  RHPFLTSLKYSFQTKDRLCFVMEYVNGGELFFHLSRERVSFSEDRTRFYGAEIVSALDYHL 121
Db  206  RHPFLTALKYSFQTHDRLCFVMEYANGGELFFHLSRERVSFSEDRARFYGAEIVSALDYHL 265

Qy  122  SGK-IVYRDLKLENLMDKDGHIKITDFGLCKEGITDAAATMKTFCGTPPEYLAPEVLEDND 180
Db  266  SEKVVYRDLKLENLMDKDGHIKITDFGLCKEGIKDGATMKTFCGTPPEYLAPEVLEDND 325

Qy  181  YGRAVDWGLGVVYEMMCGRLPFYNQDHEKLFELILMEDIKFPRTLSSDAKSLLSGLLI 240
Db  326  YGRAVDWGLGVVYEMMCGRLPFYNQDHEKLFELILMEEIRFPRTLGPPEAKSLLSGLLK 385

Qy  241  KDPNKRLLGGGPDDAKEIMRHSFFSGVNMQDVYDKLVPPFKPQVTSSTDTRYFDEE 296
Db  386  KDPKQRLGGGSEDAKEIMQHRFFAGIVMHHVYKKSPPFPKPQVTSSTDTRYFDEE 441

RESULT 9
US-09-538-092-1053
; Sequence 1053, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Giot, Ioic
; APPLICANT: Mansfield, Traci A.
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; FILE REFERENCE: 15966-542
; CURRENT APPLICATION NUMBER: US/09/538,092
; CURRENT FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/178,965
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CuratSeqFormatter Version 0.9
; SEQ ID NO 1053
; LENGTH: 480
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Polypeptide Accession Number P31749
US-09-538-092-1053

Query Match      89.2%; Score 1393.5; DB 2; Length 480;
Best Local Similarity 87.8%; Pred. No. 1.3e-124;
Matches 260; Conservative 20; Mismatches 15; Indels 1; Gaps 1;

Qy  2  TMNDFYLLKLGKGTGKVLVREKASGKYAMKILKKEVIAKDEVAHTLTESRVLKNT 61
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; GENERAL INFORMATION:
; APPLICANT: Kenneth Walsh
; APPLICANT: St. Elizabeth's Medical Center
; TITLE OF INVENTION: HMG CoA Reductase Inhibitors for
; TITLE OF INVENTION: Promoting Angiogenesis
; FILE REFERENCE: 49,784 (1417)
; CURRENT APPLICATION NUMBER: US/09/590,740
; CURRENT FILING DATE: 2000-06-08
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 480
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-590-740-2

Query Match      89.2%; Score 1393.5; DB 2; Length 480;
Best Local Similarity 87.8%; Pred. No. 1.3e-124;
Matches 260; Conservative 20; Mismatches 15; Indels 1; Gaps 1;

Qy  2  TMNDFYLLKLGKGTGKVLVREKASGKYAMKILKKEVIAKDEVAHTLTESRVLKNT 61
Db  146  TMNEFEYLKLGKGTGKVLVREKATGRYYAMKILKKEVIAKDEVAHTLTENRVLQNS 205

Qy  62  RHPFLTSLKYSFQTKDRLCFVMEYVNGGELFFHLSRERVSFSEDRTRFYGAEIVSALDYHL 121
Db  206  RHPFLTALKYSFQTHDRLCFVMEYANGGELFFHLSRERVSFSEDRARFYGAEIVSALDYHL 265

Qy  122  SGK-IVYRDLKLENLMDKDGHIKITDFGLCKEGITDAAATMKTFCGTPPEYLAPEVLEDND 180
Db  266  SEKVVYRDLKLENLMDKDGHIKITDFGLCKEGIKDGATMKTFCGTPPEYLAPEVLEDND 325

Qy  181  YGRAVDWGLGVVYEMMCGRLPFYNQDHEKLFELILMEDIKFPRTLSSDAKSLLSGLLI 240
Db  326  YGRAVDWGLGVVYEMMCGRLPFYNQDHEKLFELILMEEIRFPRTLGPPEAKSLLSGLLK 385

Qy  241  KDPNKRLLGGGPDDAKEIMRHSFFSGVNMQDVYDKLVPPFKPQVTSSTDTRYFDEE 296
Db  386  KDPKQRLGGGSEDAKEIMQHRFFAGIVMHHVYKKSPPFPKPQVTSSTDTRYFDEE 441

RESULT 10
US-09-526-043-14
; Sequence 14, Application US/09526043
; Patent No. 6881555
; GENERAL INFORMATION:
; APPLICANT: Guo, Kun
; APPLICANT: Pagnoni, Marco
; APPLICANT: Clark, Kenneth
; APPLICANT: Ivashchenko, Yuri
; TITLE OF INVENTION: AKT NUCLEIC ACIDS, POLYPEPTIDES, AND USES THEREOF
; FILE REFERENCE: A3278A-US
; CURRENT APPLICATION NUMBER: US/09/526,043
; CURRENT FILING DATE: 2000-03-14
; EARLIER APPLICATION NUMBER: 60/125,108
; EARLIER FILING DATE: 1999-03-19
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 480
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-526-043-14

Query Match      89.2%; Score 1393.5; DB 2; Length 480;
Best Local Similarity 87.8%; Pred. No. 1.3e-124;
Matches 260; Conservative 20; Mismatches 15; Indels 1; Gaps 1;

Qy  2  TMNDFYLLKLGKGTGKVLVREKASGKYAMKILKKEVIAKDEVAHTLTESRVLKNT 61
Db  146  TMNEFEYLKLGKGTGKVLVREKATGRYYAMKILKKEVIAKDEVAHTLTENRVLQNS 205

Qy  62  RHPFLTSLKYSFQTKDRLCFVMEYVNGGELFFHLSRERVSFSEDRTRFYGAEIVSALDYHL 121
Db  206  RHPFLTALKYSFQTHDRLCFVMEYANGGELFFHLSRERVSFSEDRARFYGAEIVSALDYHL 265

Qy  122  SGK-IVYRDLKLENLMDKDGHIKITDFGLCKEGITDAAATMKTFCGTPPEYLAPEVLEDND 180
Db  266  SEKVVYRDLKLENLMDKDGHIKITDFGLCKEGIKDGATMKTFCGTPPEYLAPEVLEDND 325

Qy  181  YGRAVDWGLGVVYEMMCGRLPFYNQDHEKLFELILMEDIKFPRTLSSDAKSLLSGLLI 240
Db  326  YGRAVDWGLGVVYEMMCGRLPFYNQDHEKLFELILMEEIRFPRTLGPPEAKSLLSGLLK 385

Qy  241  KDPNKRLLGGGPDDAKEIMRHSFFSGVNMQDVYDKLVPPFKPQVTSSTDTRYFDEE 296
Db  386  KDPKQRLGGGSEDAKEIMQHRFFAGIVMHHVYKKSPPFPKPQVTSSTDTRYFDEE 441

RESULT 11
US-09-771-161A-223
; Sequence 223, Application US/09771161A
; Patent No. 6936450
; GENERAL INFORMATION:
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RESULT 13

US-09-417-197-139  
; Sequence 139, Application US/09417197  
; Patent No. 6518021

```

, GENEALOGICAL INFORMATION
, APPLICANT: Ole THASTRUP, et al.
, TITLE OF INVENTION: A Method For Extracting
, TITLE OF INVENTION: On A Cellular Response
, FILE REFERENCE: 3759-0110P
, CURRENT APPLICATION NUMBER: US/09/417,197
, CURRENT FILING DATE: 1999-10-07
, NUMBER OF SEQ ID NOS: 143
, SOFTWARE: Patent In version 3.0
,

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Db 393 TMNEFEYLLKLGKTFGKVLVKEKATGRYYAMKILKKEVIVAKDEVAHTTENTRVLQNS 452

US-09-526-043-13  
 : Sequence 13, Application US/09526043  
 :  
 : Patent No. 6881555  
 : GENERAL INFORMATION:  
 :  
 : APPLICANT: Guo, Kun  
 : APPLICANT: Pagnoni, Marco  
 : APPLICANT: Clark, Kenneth  
 : APPLICANT: Ivashchenko, Yuri  
 : TITLE OF INVENTION: AKT NUCLEIC ACID

APPLICANT: Ivashchenko, Yuri

FILE REFERENCE: A3278A-US  
CURRENT APPLICATION NUMBER: US/09/526.043  
CURRENT FILING DATE: 2000-03-14  
EARLIER APPLICATION NUMBER: 60/125.108  
EARLIER FILING DATE: 1999-03-19  
NUMBER OF SEQ ID NOS: 17  
SOFTWARE: Patent in Ver. 2.1  
SEQ ID NO 13  
LENGTH: 480  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
US-09-526-043-13

Query Match 89.0%; Score 1391; DB 2; Length 480;  
Best Local Similarity 86.4%; Pred. No. 2.3e-124;  
Matches 255; Conservative 23; Mismatches 17; Indels 0; Gaps 0;

Qy 2 TMNDFVYLKLGKGTGKVLVLRKAGSKYYAMKILKEVIAKDEVAHTLTESRVLKNT 61  
Db 148 TMNDFVYLKLGKGTGKVLVLRKAGSKYYAMKILKEVIAKDEVAHTLTESRVLQNT 207

Qy 62 RHPFLTSKYSFOTKDRLCFVMEYVNGGELFFHLSRERVSFSEDRTRFYGAIVSALDYIH 121  
Db 208 RHPFLTALKYAFQTHDRLCFVMEYVNGGELFFHLSRERVSFTEERARFYGAIVSALBYLH 267

Qy 122 SGKIVYRDLEKLENMLDKDGHKIKITDFGLCKEGITDAATMKTFCGTPEYLAPEVLENDY 181  
Db 268 SRDVVYRDLEKLENMLDKDGHKIKITDFGLCKEGISDGTATMKTFCGTPEYLAPEVLENDY 327

Qy 182 GRAVDWMLGLGVVYEMMCGRLPFYNQDHEKLFELILMEDIKFPRTLSSDAKSLSLGLLIK 241  
Db 328 GRAVDWMLGLGVVYEMMCGRLPFYNQDHEKLFELILMEEIRFPRTLSPKAKSLLAGLLKK 387

Qy 242 DPNKRLGGGPDDAKEIMRHSFSGVNVQDVYDKLVPPFKPQVTSETDTRYFDEE 296  
Db 388 DPKQRLGGGSDAKEVMEHRRFLLSINWQDVVQKKLLPPFPKQVTSEVDTRYFDDDE 442

RESULT 15  
US-09-538-092-1054  
Sequence 1054, Application US/09538092  
Patent No. 6753314  
GENERAL INFORMATION:  
APPLICANT: Manfield, Traci A.  
TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same  
FILE REFERENCE: 15966-542  
CURRENT APPLICATION NUMBER: US/09/538.092  
CURRENT FILING DATE: 2000-03-29  
PRIOR APPLICATION NUMBER: 60/127,352  
PRIOR FILING DATE: 1999-04-01  
PRIOR APPLICATION NUMBER: 60/178,965  
PRIOR FILING DATE: 2000-02-01  
NUMBER OF SEQ ID NOS: 1387  
SOFTWARE: CurapatSeqFormatter Version 0.9  
SEQ ID NO 1054  
LENGTH: 481  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (0)...(0)  
OTHER INFORMATION: Polypeptide Accession Number P31751  
US-09-538-092-1054

Query Match 89.0%; Score 1391; DB 2; Length 481;  
Best Local Similarity 86.4%; Pred. No. 2.3e-124;  
Matches 255; Conservative 23; Mismatches 17; Indels 0; Gaps 0;

Qy 2 TMNDFVYLKLGKGTGKVLVLRKAGSKYYAMKILKEVIAKDEVAHTLTESRVLKNT 61  
Db 148 TMNDFVYLKLGKGTGKVLVLRKAGSKYYAMKILKEVIAKDEVAHTLTESRVLQNT 207

Qy 62 RHPFLTSKYSFOTKDRLCFVMEYVNGGELFFHLSRERVSFSEDRTRFYGAIVSALDYIH 121  
Db 208 RHPFLTALKYAFQTHDRLCFVMEYVNGGELFFHLSRERVSFTEERARFYGAIVSALBYLH 267

Qy 122 SGKIVYRDLEKLENMLDKDGHKIKITDFGLCKEGITDAATMKTFCGTPEYLAPEVLENDY 181  
Db 268 SRDVVYRDLEKLENMLDKDGHKIKITDFGLCKEGISDGTATMKTFCGTPEYLAPEVLENDY 327

Qy 182 GRAVDWMLGLGVVYEMMCGRLPFYNQDHEKLFELILMEDIKFPRTLSSDAKSLSLGLLIK 241  
Db 328 GRAVDWMLGLGVVYEMMCGRLPFYNQDHEKLFELILMEEIRFPRTLSPKAKSLLAGLLKK 387

Qy 242 DPNKRLGGGPDDAKEIMRHSFSGVNVQDVYDKLVPPFKPQVTSETDTRYFDEE 296  
Db 388 DPKQRLGGGSDAKEVMEHRRFLLSINWQDVVQKKLLPPFPKQVTSEVDTRYFDDDE 442

Search completed: February 13, 2006, 06:43:19  
Job time : 74 secs

Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	1563	100.0	465	3	US-09-526-043-2	Sequence 2, Appli
2	1563	100.0	465	4	US-10-394-568-2	Sequence 2, Appli
3	1563	100.0	465	4	US-10-394-568-12	Sequence 12, Appli
4	1563	100.0	465	6	US-11-063-691-2	Sequence 2, Appli
5	1563	100.0	479	3	US-09-771-161A-246	Sequence 246, App
6	1563	100.0	479	3	US-09-771-161A-247	Sequence 247, App
7	1563	100.0	479	3	US-09-771-161A-248	Sequence 248, App
8	1563	100.0	479	4	US-10-394-322A-3	Sequence 3, Appli
9	1563	100.0	479	4	US-10-217-574-33	Sequence 33, Appli
10	1563	100.0	479	4	US-10-217-555-33	Sequence 33, Appli
11	1563	100.0	479	5	US-10-753-267-108	Sequence 108, App
12	1558	99.7	454	3	US-09-526-043-17	Sequence 17, Appli
13	1558	99.7	454	6	US-11-063-691-17	Sequence 17, Appli
14	1394.5	89.2	320	4	US-10-116-722A-5	Sequence 5, Appli
15	1394.5	89.2	480	4	US-10-713-678-6	Sequence 6, Appli
16	1394.5	89.2	501	5	US-10-732-923-10650	Sequence 10650, A
17	1394.5	89.2	763	5	US-10-732-923-10649	Sequence 10649, A
18	1393.5	89.2	320	4	US-10-116-722A-7	Sequence 7, Appli
19	1393.5	89.2	480	3	US-09-771-161A-223	Sequence 223, App
20	1393.5	89.2	480	3	US-09-970-000-4	Sequence 4, Appli
21	1393.5	89.2	480	3	US-09-526-043-14	Sequence 14, Appli
22	1393.5	89.2	480	4	US-10-060-065-18	Sequence 18, Appli
23	1393.5	89.2	480	4	US-10-059-585-39	Sequence 39, Appli
24	1393.5	89.2	480	4	US-10-394-322A-1	Sequence 1, Appli
25	1393.5	89.2	480	4	US-10-217-574-31	Sequence 31, Appli
26	1393.5	89.2	480	4	US-10-217-555-31	Sequence 31, Appli
27	1393.5	89.2	480	4	US-10-701-490-4	Sequence 4, Appli

; Sequence 2, Application US/10394568  
; Publication No. US20040002136A1  
; GENERAL INFORMATION:  
; APPLICANT: GUO, KUN  
; APPLICANT: IVASHCHENKO, YURI  
; APPLICANT: CLARK, KENNETH L.  
; TITLE OF INVENTION: INDUCTION OF VASCULAR ENDOTHELIAL GROWTH FACTOR (VEGF)  
; TITLE OF INVENTION: BY THE SERINE/THREONINE PROTEIN KINASE AKT  
; FILE REFERENCE: A33990  
; CURRENT APPLICATION NUMBER: US/10/394,568  
; CURRENT FILING DATE: 2003-03-21  
; PRIOR APPLICATION NUMBER: US/09/584,938  
; PRIOR FILING DATE: 2000-06-01  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 465  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-394-568-2

Query Match 100.0%; Score 1563; DB 4; Length 465;  
Best Local Similarity 100.0%; Pred. No. 2.1e-111;  
Matches 296; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 KTWNDFYLLKLGKTFGKVLVREKASGKYAMKILKKEVIIAKDEVAHTLTESRVLKN 60  
Db 143 KTWNDFYLLKLGKTFGKVLVREKASGKYAMKILKKEVIIAKDEVAHTLTESRVLKN 202  
  
Qy 61 TRHPFLTSLKYSFQTKDRLCFVMEYVNGGELFFHLSRERVSFSDRTFRFYGAIEVSALDYL 120  
Db 203 TRHPFLTSLKYSFQTKDRLCFVMEYVNGGELFFHLSRERVSFSDRTFRFYGAIEVSALDYL 262  
  
Qy 121 HSGKIVYRDLKLENMLDKDGHIKITDFGLCKEGITDAATMKTFCGTPPEYLAPEVLEDND 180  
Db 263 HSGKIVYRDLKLENMLDKDGHIKITDFGLCKEGITDAATMKTFCGTPPEYLAPEVLEDND 322  
  
Qy 181 YGRAVDWMLGVVYEMMCGRLPFYNQDHEKLFELILMEDIKFPRTLSDDAKSLLSGLLI 240  
Db 323 YGRAVDWMLGVVYEMMCGRLPFYNQDHEKLFELILMEDIKFPRTLSDDAKSLLSGLLI 382  
  
Qy 241 KDPNKRLLGGGPDDAKEIMRHSFFSGVNWQDVYDKLVPPFPKQVTSFDTTRYFDEE 296  
Db 383 KDPNKRLLGGGPDDAKEIMRHSFFSGVNWQDVYDKLVPPFPKQVTSFDTTRYFDEE 438

RESULT 3  
US-10-394-568-12  
; Sequence 12, Application US/10394568  
; Publication No. US20040002136A1  
; GENERAL INFORMATION:  
; APPLICANT: GUO, KUN  
; APPLICANT: IVASHCHENKO, YURI  
; APPLICANT: CLARK, KENNETH L.  
; TITLE OF INVENTION: INDUCTION OF VASCULAR ENDOTHELIAL GROWTH FACTOR (VEGF)  
; TITLE OF INVENTION: BY THE SERINE/THREONINE PROTEIN KINASE AKT  
; FILE REFERENCE: A33990  
; CURRENT APPLICATION NUMBER: US/10/394,568  
; CURRENT FILING DATE: 2003-03-21  
; PRIOR APPLICATION NUMBER: US/09/584,938  
; PRIOR FILING DATE: 2000-06-01  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 12  
; LENGTH: 465  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-394-568-12

Query Match 100.0%; Score 1563; DB 4; Length 465;  
Best Local Similarity 100.0%; Pred. No. 2.1e-111;  
Matches 296; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KTWNDFYLLKLGKTFGKVLVREKASGKYAMKILKKEVIIAKDEVAHTLTESRVLKN 60  
Db 143 KTWNDFYLLKLGKTFGKVLVREKASGKYAMKILKKEVIIAKDEVAHTLTESRVLKN 202  
  
Qy 61 TRHPFLTSLKYSFQTKDRLCFVMEYVNGGELFFHLSRERVSFSDRTFRFYGAIEVSALDYL 120  
Db 203 TRHPFLTSLKYSFQTKDRLCFVMEYVNGGELFFHLSRERVSFSDRTFRFYGAIEVSALDYL 262  
  
Qy 121 HSGKIVYRDLKLENMLDKDGHIKITDFGLCKEGITDAATMKTFCGTPPEYLAPEVLEDND 180  
Db 263 HSGKIVYRDLKLENMLDKDGHIKITDFGLCKEGITDAATMKTFCGTPPEYLAPEVLEDND 322  
  
Qy 181 YGRAVDWMLGVVYEMMCGRLPFYNQDHEKLFELILMEDIKFPRTLSDDAKSLLSGLLI 240  
Db 323 YGRAVDWMLGVVYEMMCGRLPFYNQDHEKLFELILMEDIKFPRTLSDDAKSLLSGLLI 382  
  
Qy 241 KDPNKRLLGGGPDDAKEIMRHSFFSGVNWQDVYDKLVPPFPKQVTSFDTTRYFDEE 296  
Db 383 KDPNKRLLGGGPDDAKEIMRHSFFSGVNWQDVYDKLVPPFPKQVTSFDTTRYFDEE 438

RESULT 4  
US-11-063-691-2  
; Sequence 2, Application US/11063691  
; Publication No. US20050142603A1  
; GENERAL INFORMATION:  
; APPLICANT: Guo, Kun  
; APPLICANT: Pagnoni, Marco  
; APPLICANT: Clark, Kenneth  
; APPLICANT: Ivashchenko, Yuri  
; TITLE OF INVENTION: AKT NUCLEIC ACIDS, POLYPEPTIDES, AND USES THEREOF  
; FILE REFERENCE: A3278A-US  
; CURRENT APPLICATION NUMBER: US/11/063,691  
; CURRENT FILING DATE: 2005-02-23  
; PRIOR APPLICATION NUMBER: US/09/526,043  
; PRIOR FILING DATE: 2000-03-14  
; PRIOR APPLICATION NUMBER: 60/125,108  
; PRIOR FILING DATE: 1999-03-19  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 465  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-063-691-2

Query Match 100.0%; Score 1563; DB 6; Length 465;  
Best Local Similarity 100.0%; Pred. No. 2.1e-111;  
Matches 296; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KTWNDFYLLKLGKTFGKVLVREKASGKYAMKILKKEVIIAKDEVAHTLTESRVLKN 60  
Db 143 KTWNDFYLLKLGKTFGKVLVREKASGKYAMKILKKEVIIAKDEVAHTLTESRVLKN 202  
  
Qy 61 TRHPFLTSLKYSFQTKDRLCFVMEYVNGGELFFHLSRERVSFSDRTFRFYGAIEVSALDYL 120  
Db 203 TRHPFLTSLKYSFQTKDRLCFVMEYVNGGELFFHLSRERVSFSDRTFRFYGAIEVSALDYL 262  
  
Qy 121 HSGKIVYRDLKLENMLDKDGHIKITDFGLCKEGITDAATMKTFCGTPPEYLAPEVLEDND 180  
Db 263 HSGKIVYRDLKLENMLDKDGHIKITDFGLCKEGITDAATMKTFCGTPPEYLAPEVLEDND 322  
  
Qy 181 YGRAVDWMLGVVYEMMCGRLPFYNQDHEKLFELILMEDIKFPRTLSDDAKSLLSGLLI 240  
Db 323 YGRAVDWMLGVVYEMMCGRLPFYNQDHEKLFELILMEDIKFPRTLSDDAKSLLSGLLI 382  
  
Qy 241 KDPNKRLLGGGPDDAKEIMRHSFFSGVNWQDVYDKLVPPFPKQVTSFDTTRYFDEE 296  
Db 383 KDPNKRLLGGGPDDAKEIMRHSFFSGVNWQDVYDKLVPPFPKQVTSFDTTRYFDEE 438

RESULT 5  
US-09-771-161A-246

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; Sequence 246, Application US/09771161A
; Patent No. US20020110811A1
; GENERAL INFORMATION:
; APPLICANT: LEVINE, et al.
; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
; FILE REFERENCE: 802620-2005.1
; CURRENT APPLICATION NUMBER: US/09/771,161A
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 09/724,676
; PRIOR FILING DATE: 2000-11-28
; PRIOR FILING DATE: 2000-06-15
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 135619
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 273
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 246
; LENGTH: 479
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-771-161A-246

Query Match      100.0%; Score 1563; DB 3; Length 479;
Best Local Similarity 100.0%; Pred. No. 2.le-111;
Matches 296; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KTMNDFYLLKLGKGTGKVIIVREKASGKYAMKILKKEVIIAKDEVAHTLTESRVLKN 60
DB 143 KTMNDFYLLKLGKGTGKVIIVREKASGKYAMKILKKEVIIAKDEVAHTLTESRVLKN 202

QY 61 TRHPFLTSKYSFQTKDRLCFVMEYVNGGELFFHLSRERVSEDRTRFYGAIVSALDYL 120
DB 203 TRHPFLTSKYSFQTKDRLCFVMEYVNGGELFFHLSRERVSEDRTRFYGAIVSALDYL 262

QY 121 HSGKIVYRDLEKLEMLDKDGHIKITDFGLCKEGITDAATMKTFCGTPYLAPEVLEND 180
DB 263 HSGKIVYRDLEKLEMLDKDGHIKITDFGLCKEGITDAATMKTFCGTPYLAPEVLEND 322

QY 181 YGRAVDWMGLGVVMYEMMCGRLPFYQNDHEKLFELILMEDIKFPRRTLSSDAKSLLSGLLI 240
DB 323 YGRAVDWMGLGVVMYEMMCGRLPFYQNDHEKLFELILMEDIKFPRRTLSSDAKSLLSGLLI 382

QY 241 KDPNKRLLGGGPDDAKEIMRHSFFSGVNWQDVYDKLVPPFPKQVTSSETDTRYFDEE 296
DB 383 KDPNKRLLGGGPDDAKEIMRHSFFSGVNWQDVYDKLVPPFPKQVTSSETDTRYFDEE 438

RESULT 6
US-09-771-161A-247
; Sequence 247, Application US/09771161A
; Patent No. US20020110811A1
; GENERAL INFORMATION:
; APPLICANT: LEVINE, et al.
; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
; FILE REFERENCE: 802620-2005.1
; CURRENT APPLICATION NUMBER: US/09/771,161A
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 09/724,676
; PRIOR FILING DATE: 2000-11-28
; PRIOR FILING DATE: 2000-06-15
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 135619
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 273
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 247
; LENGTH: 479
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-771-161A-247

Query Match      100.0%; Score 1563; DB 3; Length 479;
Best Local Similarity 100.0%; Pred. No. 2.le-111;
Matches 296; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KTMNDFYLLKLGKGTGKVIIVREKASGKYAMKILKKEVIIAKDEVAHTLTESRVLKN 60
DB 143 KTMNDFYLLKLGKGTGKVIIVREKASGKYAMKILKKEVIIAKDEVAHTLTESRVLKN 202

QY 61 TRHPFLTSKYSFQTKDRLCFVMEYVNGGELFFHLSRERVSEDRTRFYGAIVSALDYL 120
DB 203 TRHPFLTSKYSFQTKDRLCFVMEYVNGGELFFHLSRERVSEDRTRFYGAIVSALDYL 262

QY 121 HSGKIVYRDLEKLEMLDKDGHIKITDFGLCKEGITDAATMKTFCGTPYLAPEVLEND 180
DB 263 HSGKIVYRDLEKLEMLDKDGHIKITDFGLCKEGITDAATMKTFCGTPYLAPEVLEND 322

QY 181 YGRAVDWMGLGVVMYEMMCGRLPFYQNDHEKLFELILMEDIKFPRRTLSSDAKSLLSGLLI 240
DB 323 YGRAVDWMGLGVVMYEMMCGRLPFYQNDHEKLFELILMEDIKFPRRTLSSDAKSLLSGLLI 382

QY 241 KDPNKRLLGGGPDDAKEIMRHSFFSGVNWQDVYDKLVPPFPKQVTSSETDTRYFDEE 296
DB 383 KDPNKRLLGGGPDDAKEIMRHSFFSGVNWQDVYDKLVPPFPKQVTSSETDTRYFDEE 438

RESULT 7
US-09-771-161A-248
; Sequence 248, Application US/09771161A
; Patent No. US20020110811A1
; GENERAL INFORMATION:
; APPLICANT: LEVINE, et al.
; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
; FILE REFERENCE: 802620-2005.1
; CURRENT APPLICATION NUMBER: US/09/771,161A
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 09/724,676
; PRIOR FILING DATE: 2000-11-28
; PRIOR FILING DATE: 2000-06-15
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 135619
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 273
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 248
; LENGTH: 479
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-771-161A-248

Query Match      100.0%; Score 1563; DB 3; Length 479;
Best Local Similarity 100.0%; Pred. No. 2.le-111;
Matches 296; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KTMNDFYLLKLGKGTGKVIIVREKASGKYAMKILKKEVIIAKDEVAHTLTESRVLKN 60
DB 143 KTMNDFYLLKLGKGTGKVIIVREKASGKYAMKILKKEVIIAKDEVAHTLTESRVLKN 202

QY 61 TRHPFLTSKYSFQTKDRLCFVMEYVNGGELFFHLSRERVSEDRTRFYGAIVSALDYL 120
DB 203 TRHPFLTSKYSFQTKDRLCFVMEYVNGGELFFHLSRERVSEDRTRFYGAIVSALDYL 262

QY 121 HSGKIVYRDLEKLEMLDKDGHIKITDFGLCKEGITDAATMKTFCGTPYLAPEVLEND 180
DB 263 HSGKIVYRDLEKLEMLDKDGHIKITDFGLCKEGITDAATMKTFCGTPYLAPEVLEND 322

QY 181 YGRAVDWMGLGVVMYEMMCGRLPFYQNDHEKLFELILMEDIKFPRRTLSSDAKSLLSGLLI 240
DB 323 YGRAVDWMGLGVVMYEMMCGRLPFYQNDHEKLFELILMEDIKFPRRTLSSDAKSLLSGLLI 382

QY 241 KDPNKRLLGGGPDDAKEIMRHSFFSGVNWQDVYDKLVPPFPKQVTSSETDTRYFDEE 296
DB 383 KDPNKRLLGGGPDDAKEIMRHSFFSGVNWQDVYDKLVPPFPKQVTSSETDTRYFDEE 438

RESULT 8
US-09-771-161A-249
; Sequence 249, Application US/09771161A
; Patent No. US20020110811A1
; GENERAL INFORMATION:
; APPLICANT: LEVINE, et al.
; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
; FILE REFERENCE: 802620-2005.1
; CURRENT APPLICATION NUMBER: US/09/771,161A
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 09/724,676
; PRIOR FILING DATE: 2000-11-28
; PRIOR FILING DATE: 2000-06-15
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 135619
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 273
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 249
; LENGTH: 479
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-771-161A-249

Query Match      100.0%; Score 1563; DB 3; Length 479;
Best Local Similarity 100.0%; Pred. No. 2.le-111;
Matches 296; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KTMNDFYLLKLGKGTGKVIIVREKASGKYAMKILKKEVIIAKDEVAHTLTESRVLKN 60
DB 143 KTMNDFYLLKLGKGTGKVIIVREKASGKYAMKILKKEVIIAKDEVAHTLTESRVLKN 202

QY 61 TRHPFLTSKYSFQTKDRLCFVMEYVNGGELFFHLSRERVSEDRTRFYGAIVSALDYL 120
DB 203 TRHPFLTSKYSFQTKDRLCFVMEYVNGGELFFHLSRERVSEDRTRFYGAIVSALDYL 262

QY 121 HSGKIVYRDLEKLEMLDKDGHIKITDFGLCKEGITDAATMKTFCGTPYLAPEVLEND 180
DB 263 HSGKIVYRDLEKLEMLDKDGHIKITDFGLCKEGITDAATMKTFCGTPYLAPEVLEND 322

QY 181 YGRAVDWMGLGVVMYEMMCGRLPFYQNDHEKLFELILMEDIKFPRRTLSSDAKSLLSGLLI 240
DB 323 YGRAVDWMGLGVVMYEMMCGRLPFYQNDHEKLFELILMEDIKFPRRTLSSDAKSLLSGLLI 382

QY 241 KDPNKRLLGGGPDDAKEIMRHSFFSGVNWQDVYDKLVPPFPKQVTSSETDTRYFDEE 296
DB 383 KDPNKRLLGGGPDDAKEIMRHSFFSGVNWQDVYDKLVPPFPKQVTSSETDTRYFDEE 438
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US-10-394-322A-3
; Sequence 3, Application US/10394322A
; Publication No. US20030232391A1
; GENERAL INFORMATION:
; APPLICANT: SUNESIS PHARMACEUTICALS, INC.
; APPLICANT: Prescott, John C.
; TITLE OF INVENTION: IDENTIFICATION OF KINASE INHIBITORS
; FILE REFERENCE: 39750-0006 US
; CURRENT FILING DATE: 2003-03-20
; PRIOR FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: US 60/366,892
; PRIOR FILING DATE: 2002-03-21
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 479
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-394-322A-3

Query Match      100.0%; Score 1563; DB 4; Length 479;
Best Local Similarity 100.0%; Pred. No. 2.1e-111;
Matches 296; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KTMNDFYLLKLGKGTGKVLVREKASGKYAMKILKKEVIIAKDEVAHTLTESRVLKN 60
Db 143 KTMNDFYLLKLGKGTGKVLVREKASGKYAMKILKKEVIIAKDEVAHTLTESRVLKN 202

Qy 61 TRHPFLTSLKYSFQTKDRLCFVMEYVNGGELFFHLSRERFSEDRTRFYGAIEVSALDYL 120
Db 203 TRHPFLTSLKYSFQTKDRLCFVMEYVNGGELFFHLSRERFSEDRTRFYGAIEVSALDYL 262

Qy 121 HSGKIVYRDLKLENLMDKDGHIKITDGLCKEGITDAATMKTFCGTPPEYLAPVLENDND 180
Db 263 HSGKIVYRDLKLENLMDKDGHIKITDGLCKEGITDAATMKTFCGTPPEYLAPVLENDND 322

Qy 181 YGRAVDWVWGLGVVYEMMCGRLPFYNQDHEKLFELILMEDIKFPRTLSSDAKSLLSGLLI 240
Db 323 YGRAVDWVWGLGVVYEMMCGRLPFYNQDHEKLFELILMEDIKFPRTLSSDAKSLLSGLLI 382

Qy 241 KDPNKRLLGGGPDDAKEIMRHSFFSGVNWQDVYDKLVPPFPKQVTSSETDTRYFDEE 296
Db 383 KDPNKRLLGGGPDDAKEIMRHSFFSGVNWQDVYDKLVPPFPKQVTSSETDTRYFDEE 438

RESULT 9
US-10-217-574-33
; Sequence 33, Application US/10217574
; Publication No. US20040005687A1
; GENERAL INFORMATION:
; APPLICANT: Barford, David
; APPLICANT: Yang, Jing
; APPLICANT: Hemmings, Brian A
; APPLICANT: Cron, Peter D
; TITLE OF INVENTION: Kinase Crystal Structures
; FILE REFERENCE: 44237
; CURRENT FILING DATE: 2002-12-23
; PRIOR FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: GB 0119860.5
; PRIOR FILING DATE: 2002-05-01
; PRIOR APPLICATION NUMBER: GB 0216215.4
; PRIOR FILING DATE: 2002-07-12
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 33
; LENGTH: 479
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-217-574-33

Query Match      100.0%; Score 1563; DB 4; Length 479;
Best Local Similarity 100.0%; Pred. No. 2.1e-111;
Matches 296; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KTMNDFYLLKLGKGTGKVLVREKASGKYAMKILKKEVIIAKDEVAHTLTESRVLKN 60
Db 143 KTMNDFYLLKLGKGTGKVLVREKASGKYAMKILKKEVIIAKDEVAHTLTESRVLKN 202

Qy 61 TRHPFLTSLKYSFQTKDRLCFVMEYVNGGELFFHLSRERFSEDRTRFYGAIEVSALDYL 120
Db 203 TRHPFLTSLKYSFQTKDRLCFVMEYVNGGELFFHLSRERFSEDRTRFYGAIEVSALDYL 262

Qy 121 HSGKIVYRDLKLENLMDKDGHIKITDGLCKEGITDAATMKTFCGTPPEYLAPVLENDND 180
Db 263 HSGKIVYRDLKLENLMDKDGHIKITDGLCKEGITDAATMKTFCGTPPEYLAPVLENDND 322

Qy 181 YGRAVDWVWGLGVVYEMMCGRLPFYNQDHEKLFELILMEDIKFPRTLSSDAKSLLSGLLI 240
Db 323 YGRAVDWVWGLGVVYEMMCGRLPFYNQDHEKLFELILMEDIKFPRTLSSDAKSLLSGLLI 382

Qy 241 KDPNKRLLGGGPDDAKEIMRHSFFSGVNWQDVYDKLVPPFPKQVTSSETDTRYFDEE 296
Db 383 KDPNKRLLGGGPDDAKEIMRHSFFSGVNWQDVYDKLVPPFPKQVTSSETDTRYFDEE 438
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Best Local Similarity 100.0%; Pred. No. 2.1e-111;
Matches 296; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KTMNDFYLLKLGKGTGKVLVREKASGKYAMKILKKEVIIAKDEVAHTLTESRVLKN 60
Db 143 KTMNDFYLLKLGKGTGKVLVREKASGKYAMKILKKEVIIAKDEVAHTLTESRVLKN 202

Qy 61 TRHPFLTSLKYSFQTKDRLCFVMEYVNGGELFFHLSRERFSEDRTRFYGAIEVSALDYL 120
Db 203 TRHPFLTSLKYSFQTKDRLCFVMEYVNGGELFFHLSRERFSEDRTRFYGAIEVSALDYL 262

Qy 121 HSGKIVYRDLKLENLMDKDGHIKITDGLCKEGITDAATMKTFCGTPPEYLAPVLENDND 180
Db 263 HSGKIVYRDLKLENLMDKDGHIKITDGLCKEGITDAATMKTFCGTPPEYLAPVLENDND 322

Qy 181 YGRAVDWVWGLGVVYEMMCGRLPFYNQDHEKLFELILMEDIKFPRTLSSDAKSLLSGLLI 240
Db 323 YGRAVDWVWGLGVVYEMMCGRLPFYNQDHEKLFELILMEDIKFPRTLSSDAKSLLSGLLI 382

Qy 241 KDPNKRLLGGGPDDAKEIMRHSFFSGVNWQDVYDKLVPPFPKQVTSSETDTRYFDEE 296
Db 383 KDPNKRLLGGGPDDAKEIMRHSFFSGVNWQDVYDKLVPPFPKQVTSSETDTRYFDEE 438

RESULT 10
US-10-217-555-33
; Sequence 33, Application US/10217555
; Publication No. US20040009569A1
; GENERAL INFORMATION:
; APPLICANT: Barford, David
; APPLICANT: Yang, Jing
; APPLICANT: Hemmings, Brian A
; APPLICANT: Cron, Peter D
; TITLE OF INVENTION: Kinase Crystal Structures and Materials and Methods for
; TITLE OF INVENTION: Kinase Activation
; FILE REFERENCE: 44236
; CURRENT FILING DATE: 2002-12-23
; CURRENT FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: GB 0119860.5
; PRIOR FILING DATE: 2001-08-14
; PRIOR APPLICATION NUMBER: GB 0209985.1
; PRIOR FILING DATE: 2002-05-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 33
; LENGTH: 479
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-217-555-33

Query Match      100.0%; Score 1563; DB 4; Length 479;
Best Local Similarity 100.0%; Pred. No. 2.1e-111;
Matches 296; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KTMNDFYLLKLGKGTGKVLVREKASGKYAMKILKKEVIIAKDEVAHTLTESRVLKN 60
Db 143 KTMNDFYLLKLGKGTGKVLVREKASGKYAMKILKKEVIIAKDEVAHTLTESRVLKN 202

Qy 61 TRHPFLTSLKYSFQTKDRLCFVMEYVNGGELFFHLSRERFSEDRTRFYGAIEVSALDYL 120
Db 203 TRHPFLTSLKYSFQTKDRLCFVMEYVNGGELFFHLSRERFSEDRTRFYGAIEVSALDYL 262

Qy 121 HSGKIVYRDLKLENLMDKDGHIKITDGLCKEGITDAATMKTFCGTPPEYLAPVLENDND 180
Db 263 HSGKIVYRDLKLENLMDKDGHIKITDGLCKEGITDAATMKTFCGTPPEYLAPVLENDND 322

Qy 181 YGRAVDWVWGLGVVYEMMCGRLPFYNQDHEKLFELILMEDIKFPRTLSSDAKSLLSGLLI 240
Db 323 YGRAVDWVWGLGVVYEMMCGRLPFYNQDHEKLFELILMEDIKFPRTLSSDAKSLLSGLLI 382

Qy 241 KDPNKRLLGGGPDDAKEIMRHSFFSGVNWQDVYDKLVPPFPKQVTSSETDTRYFDEE 296
Db 383 KDPNKRLLGGGPDDAKEIMRHSFFSGVNWQDVYDKLVPPFPKQVTSSETDTRYFDEE 438
```

## RESULT 11

US-10-753-267-108  
; Sequence 108, Application US/10753267  
; Publication No. US20050037946A1  
; GENERAL INFORMATION:  
; APPLICANT: Millennium Pharmaceuticals, Inc.  
; APPLICANT: Stagliano, Nancy E.  
; APPLICANT: Healy, Aileen  
; APPLICANT: Acton, Susan L.  
; APPLICANT: Galvin, Katherine M.  
; APPLICANT: Donoghue, Mary A.  
; APPLICANT: Rodrigue-Way, Amelie  
; APPLICANT: Tomlinson, James E.  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING  
; TITLE OF INVENTION: CARDIOVASCULAR DISEASE USING 1722, 10280, 59917, 85553,  
; TITLE OF INVENTION: 10653, 9235, 21668, 17794, 2210, 6169, 10102, 21061, 17662,  
; TITLE OF INVENTION: 1468, 12282, 6350, 9035, 1820, 23652, 7301, 8925, 8701,  
; TITLE OF INVENTION: 3533, 9462, 9123, 12788, 17729, 65552, 1261, 21476, 33770,  
; TITLE OF INVENTION: 9380, 2569654, 33556, 53656, 44143, 32612, 10671, 261,  
; TITLE OF INVENTION: 44570, 41922, 2552, 2417, 19319, 43969, 8921, 8993, 955,  
; TITLE OF INVENTION: 32345, 966, 1920, 17318, 1510, 14180, 26005, 554, 16408,  
; TITLE OF INVENTION: 42028, 112091, 13886, 13942, 1673, 54946 OR 2419  
; FILE REFERENCE: MP103-003P1RQNMIM  
; CURRENT APPLICATION NUMBER: US/10/753,267  
; CURRENT FILING DATE: 2004-01-08  
; PRIOR APPLICATION NUMBER: US 60/439,683  
; PRIOR FILING DATE: 2003-01-13  
; PRIOR APPLICATION NUMBER: US 60/445,216  
; PRIOR FILING DATE: 2003-02-05  
; PRIOR APPLICATION NUMBER: US 60/448,036  
; PRIOR FILING DATE: 2003-02-18  
; PRIOR APPLICATION NUMBER: US 60/454,189  
; PRIOR FILING DATE: 2003-03-12  
; PRIOR APPLICATION NUMBER: US 60/457,541  
; PRIOR FILING DATE: 2003-03-25  
; PRIOR APPLICATION NUMBER: US 60/466,411  
; PRIOR FILING DATE: 2003-04-29  
; PRIOR APPLICATION NUMBER: US 60/469,041  
; PRIOR FILING DATE: 2003-05-08  
; PRIOR APPLICATION NUMBER: US 60/477,414  
; PRIOR FILING DATE: 2003-06-10  
; PRIOR APPLICATION NUMBER: US 60/478,560  
; PRIOR FILING DATE: 2003-06-13  
; PRIOR APPLICATION NUMBER: US 60/489,772  
; PRIOR FILING DATE: 2003-07-24  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 130  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 108  
; LENGTH: 479  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
US-10-753-267-108

Query Match 100.0%; Score 1563; DB 5; Length 479;  
Best Local Similarity 100.0%; Pred. No. 2.1e-111;  
Matches 296; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KTMNDFYLLKLGKTFGKIVLVREKASGKYAMKILKEVIAKDEVAHTLTESRVLKN 60  
DB 143 KTMNDFYLLKLGKTFGKIVLVREKASGKYAMKILKEVIAKDEVAHTLTESRVLKN 202  
QY 61 TRHPFLTSKYSFQTKDRLCFVMEYVNGGELFFHLSRERVSFSDRTFRFYGAIVSALDYL 120  
DB 203 TRHPFLTSKYSFQTKDRLCFVMEYVNGGELFFHLSRERVSFSDRTFRFYGAIVSALDYL 262  
QY 121 HSGKIVYRDLKLENMLDKDGHIKITDFGLCKEGITDAATMKTFCGTPYLAPEVLEND 180  
DB 263 HSGKIVYRDLKLENMLDKDGHIKITDFGLCKEGITDAATMKTFCGTPYLAPEVLEND 322  
QY 181 YGRAVDWGLGVVYEMMCGRLPFYVNDQHEKLFELILMEDIKFPRTLSSDAKSLLSGLLI 240

DB 323 YGRAVDWGLGVVYEMMCGRLPFYVNDQHEKLFELILMEDIKFPRTLSSDAKSLLSGLLI 382  
QY 241 KDPNKRLLGGGPDDAKEIMRHSFFSGVNWQDVYDKLVPPFKPQVTSSETDTRYFDEE 296  
DB 383 KDPNKRLLGGGPDDAKEIMRHSFFSGVNWQDVYDKLVPPFKPQVTSSETDTRYFDEE 438

## RESULT 12

US-09-526-043-17  
; Sequence 17, Application US/09526043  
; Publication No. US20030100049A1  
; GENERAL INFORMATION:  
; APPLICANT: Guo, Kun  
; APPLICANT: Pagnoni, Marco  
; APPLICANT: Clark, Kenneth  
; APPLICANT: Ivaashchenko, Yuri  
; TITLE OF INVENTION: AKT NUCLEIC ACIDS, POLYPEPTIDES, AND USES THEREOF  
; FILE REFERENCE: A3278A-US  
; CURRENT APPLICATION NUMBER: US/09/526,043  
; CURRENT FILING DATE: 2000-03-14  
; EARLIER APPLICATION NUMBER: 60/125,108  
; EARLIER FILING DATE: 1999-03-19  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 17  
; LENGTH: 454  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: PCR Primer  
US-09-526-043-17

Query Match 99.7%; Score 1558; DB 3; Length 454;  
Best Local Similarity 99.7%; Pred. No. 4.9e-111;  
Matches 295; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KTMNDFYLLKLGKTFGKIVLVREKASGKYAMKILKEVIAKDEVAHTLTESRVLKN 60  
DB 143 KTMNDFYLLKLGKTFGKIVLVREKASGKYAMKILKEVIAKDEVAHTLTESRVLKN 202  
QY 61 TRHPFLTSKYSFQTKDRLCFVMEYVNGGELFFHLSRERVSFSDRTFRFYGAIVSALDYL 120  
DB 203 TRHPFLTSKYSFQTKDRLCFVMEYVNGGELFFHLSRERVSFSDRTFRFYGAIVSALDYL 262  
QY 121 HSGKIVYRDLKLENMLDKDGHIKITDFGLCKEGITDAATMKTFCGTPYLAPEVLEND 180  
DB 263 HSGKIVYRDLKLENMLDKDGHIKITDFGLCKEGITDAATMKTFCGTPYLAPEVLEND 322  
QY 181 YGRAVDWGLGVVYEMMCGRLPFYVNDQHEKLFELILMEDIKFPRTLSSDAKSLLSGLLI 240  
DB 323 YGRAVDWGLGVVYEMMCGRLPFYVNDQHEKLFELILMEDIKFPRTLSSDAKSLLSGLLI 382  
QY 241 KDPNKRLLGGGPDDAKEIMRHSFFSGVNWQDVYDKLVPPFKPQVTSSETDTRYFDEE 296  
DB 383 KDPNKRLLGGGPDDAKEIMRHSFFSGVNWQDVYDKLVPPFKPQVTSSETDTRYFDEE 438

## RESULT 13

US-11-063-691-17  
; Sequence 17, Application US/11063691  
; Publication No. US20050142603A1  
; GENERAL INFORMATION:  
; APPLICANT: Guo, Kun  
; APPLICANT: Pagnoni, Marco  
; APPLICANT: Clark, Kenneth  
; APPLICANT: Ivaashchenko, Yuri  
; TITLE OF INVENTION: AKT NUCLEIC ACIDS, POLYPEPTIDES, AND USES THEREOF  
; FILE REFERENCE: A3278A-US  
; CURRENT APPLICATION NUMBER: US/11/063,691  
; CURRENT FILING DATE: 2005-02-23  
; PRIOR APPLICATION NUMBER: US/09/526,043  
; PRIOR FILING DATE: 2000-03-14

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; PRIOR APPLICATION NUMBER: 60/125,108
; PRIOR FILING DATE: 1999-03-19
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 454
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: PCR Primer
US-11-063-691-17

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Query Match	99.7%	Score 1558	DB 6	Length 454
Best Local Similarity	99.7%	Pred. No. 4.9e-111		
Matches 295	Conservative 0	Mismatches 1	Indels 0	Gaps 0
Qy 1	KTWNDFYLLGLGTFGKVLVREKASGKYIYAMKILKKEVIIAKDEVAHTLTESRVLKN	60		
Db 143	KTWNDFYLLGLGTFGKVLVREKASGKYIYAMKILKKEVIIAKDEVAHTLTESRVLKN	202		
Qy 61	TRHPFLTSLKYSFOTKORLCFVMEVYNGGELFFHLSRERFVSEORTFYGAETVLSADYL	120		
Db 203	TRHPFLTSLKYSFOTKORLCFVMEVYNGGELFFHLSRERFVSEORTFYGAETVLSADYL	262		
Qy 121	HSGKIVYRDLKLENLMDLKOGHIKITDPLGCKEGITDAAATMKTCGTPPEYLAPVLEDND	180		
Db 263	HSGKIVYRDLKLENLMDLKOGHIKITDPLGCKEGITDAAATMKTCGTPPEYLAPVLEDND	322		
Qy 181	YGRAVDNHWGLGVVNYEMCMGRLPFYNODHEKLFELILMEDIKFPRTLSDDAKSLLSGLLI	240		
Db 323	YGRAVDNHWGLGVVNYEMCMGRLPFYNQDHEKLFELILMEDIKFPRTLSDDAKSLLSGLLI	382		
Qy 241	KDPNKRILGGGPDDAKEINVRSHFFSGVNMQDYYDKLVPPFPKQVTSSETDTRYPDEE	296		
Db 383	KDPNKRILGGGPDDBPKETMRSHFFSGVNMQDYYDKLVPPFPKQVTSSETDTRYPDEE	438		

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RESULT 14
US-10-116-722A-5
; Sequence 5, Application US/10116722A
; Publication No. US2003004496A1
; GENERAL INFORMATION:
; APPLICANT: LONGO, VALTER D.
; TITLE OF INVENTION: GENES, MUTATIONS, AND DRUGS THAT INCREASE CELLULAR
; TITLE OF INVENTION: RESISTANCE TO DAMAGE AND EXTEND LONGEVITY IN ORGANISMS
; TITLE OF INVENTION: FROM YEAST TO HUMANS
; FILE REFERENCE: 13761-7088
; CURRENT APPLICATION NUMBER: US/10/116.722A
; CURRENT FILING DATE: 2002-10-11
; PRIOR APPLICATION NUMBER: 60/281,213
; PRIOR FILING DATE: 2001-04-03
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 320
; TYPE: PRT
; ORGANISM: Murine sp.
US-10-116-722A-5

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Query Match 89.2%; Score 1394.5; DB 4; Length 320;  
Best Local Similarity 87.8%; Pred. No. 1.1e-98;  
Matches 260; Conservative 20; Mismatches 15; Indels 1; Gaps 1;

Qy	2	TMNDFDYLLKLGKTFGKVILVRKASKKYYAMKILKKEVIAKDEVAHTTETSRVLKNT	61
		: :	
Db	9	TMNEFEYLKLKGKTFGKVILVKEKATGRYYAMKILKKEVIAKDEVAHTTETSRVLQS	68
		: :	
Qy	62	RHPPLTSIKYSFQTKDLRCFWMEVNGSELPFHLSRERVPSEDTRFYGAIEIVSALDYH	121
		: :	
Db	69	RHPPLTTALKYSFTQTHRLCFCWMEVANGSELFPHLRSRKVPSEDRARFYGAIEIVSALDYH	128
		: ~	
Qy	122	SGK-IVYRDCLKENLMDKOGHIITDFGLCKEGITDAATMKTCPTGYLAPELVLEND	180

Db	129	SEKVVYRDILKLEINMLDKOGHILITDFGLCKEGIKDGATWMTFCGTPEYLAPEVJEDND	188
Qy	181	YGRAVDWVGLGVVYEMWCMGRLLPPYNQDHEKFLPEILMEDTKPRTLSGDKAALLSGLLI	240
Db	189	YGRAVDWVGLGVVYEMWCMGRLLPPYNQDHEKFLPEILMBEIRFRTLTGPEAKLSLGLLK	248
Qy	241	KDPNKRLGGGPDDAKEIMRHSFFSGVNWQDVYDKLVPPFPQVTSSETDTRYFDEE	296
Db	249	KDPTQRLGGSGDAKEIMQIRFFANIVQDVIYEKLSPPFPQVTSSETDTRYFDEE	304

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RESULT 15
US-10-713-678-6
; Sequence 6, Application US/10713678
; Publication No. US20040122077A1
; GENERAL INFORMATION:
; APPLICANT: Kenneth Walsh
; APPLICANT: St. Elizabeth's Medical Center
; TITLE OF INVENTION: HWG CoA Reductase Inhibitors for
; TITLE OF INVENTION: Promoting Angiogenesis
; FILE REFERENCE: 49,784 (1417)
; CURRENT APPLICATION NUMBER: US/10713,678
; CURRENT FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: US/09/590,740
; PRIOR FILING DATE: 2000-06-08
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 480
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-713-678-6

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Query Match 89.2%; Score 1394.5; DB 4; Length 480;  
Best Local Similarity 87.8%; Pred. No. 1.7e-98;  
Matches 260; Conservative 20; Mismatches 15; Indels 1; Gaps 1

Qy	2	TMDFDYLLKLLGKGTFGKVLVRBKA	SGKYYAMKILKEVIAAKDEVAHTLTES	VLKMT	61
Db	146	TWNEFEYLLKLLGKGTFGKVLVRBKA	TGRYYAMKILKEVIAAKDEVAHTLTEN	VLQNS	205
Qy	62	RHPFLTSKYSFQDKRLCFVMEYVNG	ELPFHLSRERVSFSEDTRFRFYGAEIV	SALDYHL	121
Db	206	RHPFLTALKYSFQTHDRLCFVMEYV	NGGELEPFHLSRERVSFSEDRARFY	GAEIVSALDYHL	265
Qy	122	SGK-IVYRDLKLENLMDKDGHIIKIT	DFGLCKEGITDAATWKTFCGTPGYLA	PEVLEND	180
Db	266	SEKNVYRDLKLENLMDKDGHIIKIT	DFGLCKEGIKDGTWKTFCGTPGYLA	PEVLEND	325
Qy	181	YGRAVDWVLGVVNYEMMCGRLPFYN	ODHEKLFELIMEDIKFPRTLSDDAK	SLSGLLI	240
Db	326	YGRAVDWVLGVVNYEMMCGRLPFYN	QDHEKLFELIMEEIRFPRTLGP	EAKSLSLGULK	385
Qy	241	KDPNKRLLGGPDDAKEIMRHSFFSG	VNWQVYDVKLVPPFPQVTS	ETDTRFYDDE	296
Db	386	KDPTORLGGGSEDAKEIMORFFANI	VMODYEKKLSPFPQVTS	ETDTRFYDDE	441

Search completed: February 13, 2006, 07:06:07  
Job time : 282 secs



GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on: February 13, 2006, 07:01:34 ; Search time 16 Seconds  
(without alignments)  
242.767 Million cell updates/sec

Title: US-10-601-311-1\_COPY\_143\_438

Perfect score: 1563

Sequence: 1 KTMNDFYLLKLGKTFKVV.....VPPFKPQVTSIDTRYFDEE 296

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 97014 seqs, 13122538 residues

Total number of hits satisfying chosen parameters: 97014

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA New:\*

1: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB pep.\*  
2: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB pep.\*  
3: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB pep.\*  
4: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB pep.\*  
5: /cgn2\_6/ptodata/2/pubpaa/US09\_NEW\_PUB pep.\*  
6: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB pep.\*  
7: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB pep.\*  
8: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Match	Query	ID	Description
1	1393.5	89.2	480	7	US-11-109-156-18 Sequence 18, Appl
2	856	54.8	543	6	US-10-821-234-1158 Sequence 1158, Ap
3	819.5	52.4	737	7	US-11-152-366-28 Sequence 28, Appl
4	761	48.7	942	6	US-10-770-726-76 Sequence 76, Appl
5	761	48.7	942	6	US-10-329-258-16 Sequence 16, Appl
6	758.5	48.5	351	7	US-11-099-958-2 Sequence 2, Appl
7	758.5	48.5	705	6	US-10-995-561-856 Sequence 856, App
8	758.5	48.5	706	6	US-10-995-561-855 Sequence 855, App
9	758.5	48.5	706	6	US-11-099-958-1 Sequence 1, Appl
10	735	47.0	495	6	US-10-770-726-81 Sequence 81, Appl
11	720	46.1	740	6	US-10-878-556A-129 Sequence 129, App
12	686.5	43.9	351	7	US-11-132-142-13 Sequence 13, Appl
13	680.5	43.5	343	7	US-11-092-168-3 Sequence 3, Appl
14	679.5	43.5	341	7	US-11-092-168-4 Sequence 4, Appl
15	675.5	43.2	351	7	US-11-132-142-14 Sequence 14, Appl
16	675.5	43.2	462	7	US-11-132-142-10 Sequence 10, Appl
17	669.5	42.8	350	6	US-10-497-767-4 Sequence 4, Appl
18	658.5	42.1	353	7	US-11-132-142-11 Sequence 11, Appl
19	656.5	42.0	395	7	US-11-132-142-12 Sequence 12, Appl
20	656.5	42.0	548	7	US-11-132-142-5 Sequence 5, Appl
21	650	41.6	398	7	US-11-132-142-7 Sequence 7, Appl
22	636.5	40.7	515	7	US-11-132-142-8 Sequence 8, Appl
23	634.5	40.6	381	7	US-11-132-142-9 Sequence 9, Appl
24	625.5	40.0	480	7	US-11-132-142-6 Sequence 6, Appl
25	571	36.5	256	6	US-10-877-346-72 Sequence 72, Appl

Sequence 183, Appl  
Sequence 49, Appl  
Sequence 48, Appl  
Sequence 45, Appl  
Sequence 20, Appl  
Sequence 18, Appl  
Sequence 17, Appl  
Sequence 12, Appl  
Sequence 148, Appl  
Sequence 147, Appl  
Sequence 16, Appl  
Sequence 4, Appl  
Sequence 11, Appl  
Sequence 9, Appl  
Sequence 146, Appl  
Sequence 19, Appl  
Sequence 145, Appl  
Sequence 144, Appl  
Sequence 11, Appl

#### ALIGNMENTS

#### RESULT 1

US-11-109-156-18  
; Sequence 18, Application US/1109156  
; Publication No. US20050250144A1  
; GENERAL INFORMATION:  
; APPLICANT: Toshio Ota  
; APPLICANT: Takao Isogai  
; APPLICANT: Tetsuo Nishikawa  
; APPLICANT: Koji Hayashi  
; APPLICANT: Kaoru Otsuka  
; APPLICANT: Jun-ichi Yamamoto  
; APPLICANT: Shizuko Ishii  
; APPLICANT: Tomoyasu Sugiyama  
; APPLICANT: Ai Wakamatsu  
; APPLICANT: Keiichi Nagai  
; APPLICANT: Tetsuji Otsuki  
; APPLICANT: Shin-ichi Funahashi  
; APPLICANT: Chitaki Senoo  
; APPLICANT: Jun-ichi Nezu  
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEIN KINASE/PROTEIN  
; FILE REFERENCE: 06501-099002  
; CURRENT APPLICATION NUMBER: US/11/109,156  
; CURRENT FILING DATE: 2005-04-19  
; PRIOR APPLICATION NUMBER: US/10/060,065  
; PRIOR FILING DATE: 2002-01-29  
; PRIOR APPLICATION NUMBER: PCT/JP00/05061  
; PRIOR FILING DATE: 2000-07-28  
; PRIOR APPLICATION NUMBER: US 60/159,590  
; PRIOR FILING DATE: 1999-10-18  
; PRIOR APPLICATION NUMBER: US 60/183,322  
; PRIOR FILING DATE: 2000-02-17  
; PRIOR APPLICATION NUMBER: JP 11-248036  
; PRIOR FILING DATE: 1999-07-29  
; PRIOR APPLICATION NUMBER: JP 2000-118776  
; PRIOR FILING DATE: 2000-01-11  
; PRIOR APPLICATION NUMBER: JP 2000-183767  
; PRIOR FILING DATE: 2000-05-02  
; PRIOR APPLICATION NUMBER: JP 2000-241899  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 18  
; LENGTH: 480  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-109-156-18

Query Match 89.2%; Score 1393.5; DB 7; Length 480;  
Best Local Similarity 87.8%; Pred. No. 1.7e-113;  
Matches 260; Conservative 20; Mismatches 15; Indels 1; Gaps 1;

Qy 2 TMNDFYLLKLGKTFGKVIILVREKASGYAMKILKEVIIAKDEVAHTLTESRVLNKT 61  
Db TMEFEYLLKLGKTFGKVIILVREKATGRYYAMKILKEVIAKDEVAHTLTENRVLQNS 205  
Qy 62 RHPFLTSLKYSFQTKDRLCFVMEYVNGELFFHLSRERVSEDRTRFYGAIEIVSALDYH 121  
Db 206 RHPFLTALKYSFQTHDLCLCFVMEYANGELFFHLSRERVSEDRARFYGAIEIVSALDYH 265  
Qy 122 SGK-IVYRDLEKLENMLDKGHIKITDFGLCKEGITDAATMKTFCGTPPEYLAPEVLBN 180  
Db 266 SEKNVYRDLEKLENMLDKGHIKITDFGLCKEGIKDGATMKTFCGTPPEYLAPEVLBN 325  
Qy 181 YGRAVDWGLGVVYEMMCGRLPFYNQDHEKLFELIIMEDIKFPRTLSSDAKSLGLLI 240  
Db 326 YGRAVDWGLGVVYEMMCGRLPFYNQDHEKLFELIIMEDIKFPRTLSSDAKSLGLLI 385  
Qy 241 KDPNKRLLGGGPDDAKEMRHSFFSGVNWQDVYDKLVPPPKPQVTSSETDTRYFDEE 296  
Db 386 KDPKRLGGGSDAKEMRHSFFAGIVQHVYKSLSPFPKQVTSSETDTRYFDEE 441

RESULT 2  
US-10-821-234-1158  
; Sequence 1158, Application US/10821234  
; Publication No. US200502551141  
; GENERAL INFORMATION:  
; APPLICANT: Labat, Ivan  
; APPLICANT: Stache-Crain, Birgit  
; APPLICANT: Andarmani, Susan  
; APPLICANT: Tang, Y. Tom  
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia  
; FILE REFERENCE: 821A  
; CURRENT APPLICATION NUMBER: US/10/821.234  
; CURRENT FILING DATE: 2004-04-07  
; PRIOR APPLICATION NUMBER: US 60/462, 047  
; PRIOR FILING DATE: 2003-04-07  
; NUMBER OF SEQ ID NOS: 1704  
; SOFTWARE: pc\_seq\_genes version 1.0  
; SEQ ID NO 1158  
; LENGTH: 543  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-821-234-1158

Query Match 54.8%; Score 856; DB 6; Length 543;  
Best Local Similarity 54.8%; Pred. No. 7.8e-67;  
Matches 161; Conservative 47; Mismatches 84; Indels 2; Gaps 2;

Qy 4 NDFYLLKLGKTFGKVIILVREKASGYAMKILKEVIIAKDEVAHTLTESRV-LKNTR 62  
Db 208 SDFHFLKVIKSGFGKVIILVREKAEVYAVKVLQKAILKKKEKHIMSERNVLLKNVK 267  
Qy 63 HPFLTSLKYSFQTKDRLCFVMEYVNGELFFHLSRERVSEDRTRFYGAIEIVSALDYH 122  
Db 268 HPFLVGLHFSQTKADKLVYLDYINGELFFHLSRERVSEDRTRFYGAIEIVSALDYH 327  
Qy 123 GKIVYRDLEKLENMLDKGHIKITDFGLCKEGITDAATMKTFCGTPPEYLAPEVLBN 182  
Db 328 LNIYVYRDLEKLENMLDKGHIKITDFGLCKEGITDAATMKTFCGTPPEYLAPEVLBN 387  
Qy 183 RAVDWGLGVVYEMMCGRLPFYNQDHEKLFELIIMEDIKFPRTLSSDAKSLGLLI 242  
Db 388 RTVDWGLGVVYEMMCGRLPFYNQDHEKLFELIIMEDIKFPRTLSSDAKSLGLLI 447  
Qy 243 PNKRLGGGPDDAKEMRHSFFSGVNWQDVYDKLVPPPKPQVTSSETDTRYFDEE 296  
Db 448 RTKRL-GAKDDFMEIKSHVFFSLINWDDLINLKNKLTTPFPNPNVSGNDLRHFDPE 500

RESULT 3  
US-11-152-366-28  
; Sequence 28, Application US/11152366  
; Publication No. US20060014184A1  
; GENERAL INFORMATION:  
; APPLICANT: Brys, Reginald  
; APPLICANT: Vandeghinste, Nick  
; APPLICANT: Tomme, Peter H. M.  
; TITLE OF INVENTION: Treatment Of Degenerative & Inflammatory Diseases  
; FILE REFERENCE: P27,880-A USA  
; CURRENT APPLICATION NUMBER: US/11/152,366  
; CURRENT FILING DATE: 2005-06-14  
; PRIOR APPLICATION NUMBER: 60/579,307  
; PRIOR FILING DATE: 2004-06-14  
; NUMBER OF SEQ ID NOS: 295  
; SOFTWARE: Patentin version 3.3  
; SEQ ID NO 28  
; LENGTH: 737  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-152-366-28

Query Match 52.4%; Score 819.5; DB 7; Length 737;  
Best Local Similarity 50.0%; Pred. No. 1.7e-63;  
Matches 150; Conservative 62; Mismatches 79; Indels 9; Gaps 3;

Qy 3 MNDFYLLKLGKTFGKVIILVREKASGYAMKILKEVIIAKDEVAHTLTESRVLNKT 62  
Db 405 LDFNFYLLKLGKTFGKVIILVREKAEVYAVKVLQKAILKKKEKHIMSERNVLLKNVK 464  
Qy 63 HPFLTSLKYSFQTKDRLCFVMEYVNGELFFHLSRERVSEDRTRFYGAIEIVSALDYH 121  
Db 465 KHPYLTQLYCCFQTKDRLCFVMEYVNGELFFHLSRERVSEDRTRFYGAIEIVSALDYH 524  
Qy 122 SGKIVYRDLEKLENMLDKGHIKITDFGLCKEGITDAATMKTFCGTPPEYLAPEVLBN 181  
Db 525 QHGVYVYRDLEKLENMLDKGHIKITDFGLCKEGITDAATMKTFCGTPPEYLAPEVLBN 584  
Qy 182 GRAVDWGLGVVYEMMCGRLPFYNQDHEKLFELIIMEDIKFPRTLSSDAKSLGLLI 241  
Db 585 GPSVDWGLGVVYEMMCGRLPFYNQDHEKLFELIIMEDIKFPRTLSSDAKSLGLLI 644  
Qy 242 DPNKRLG-----GGPDDAKEMRHSFFSGVNWQDVYDKLVPPPKPQVTSSETDTRYFDEE 296  
Db 645 NPHKRLGCVASQNGEDAIIQ---HPPFKEIDWLVLEQKKIKPPFKPRIKTRDWNVNFDD 701

RESULT 4  
US-10-770-726-76  
; Sequence 76, Application US/10770726  
; Publication No. US20050266409A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Brown, Eugene  
; APPLICANT: Liu, Wei  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING, PREVENTING, AND TREATING  
; FILE REFERENCE: AM101079 (031896-010000)  
; CURRENT APPLICATION NUMBER: US/10/770,726  
; CURRENT FILING DATE: 2004-02-04  
; NUMBER OF SEQ ID NOS: 48640  
; SOFTWARE: Patentin version 3.2  
; SEQ ID NO 76  
; LENGTH: 942  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-770-726-76

Query Match 48.7%; Score 761; DB 6; Length 942;  
Best Local Similarity 48.0%; Pred. No. 2.7e-58;  
Matches 143; Conservative 59; Mismatches 92; Indels 4; Gaps 2;







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; 2004-09-09
; 2003-10-14
; 2003-10-14
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 343
; TYPE: PRT
; ORGANISM: Bos taurus
US-11-092-168-3
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Query Match 43.5%; Score 680.5; DB 7; Length 343;
Best Local Similarity 44.4%; Pred. No. 7.1e-52;
Matches 131; Conservative 53; Mismatches 104; Indels 7; Gaps 2;
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Qy 3 MNDPDLKLLGKGTGKGVILVREKASGYAMKILKEVIAKDEVAHTLTESVILKNTNR 62
Db 33 LDQFERIKTLTGSGFGRVLMVKHETGNHFAWKILDKQKVVKLQKQIEHTLNEKRILQAVN 92
Qy 63 HPFLTSLKYSFQTKDRLCFVMEYVNGGELFPHLSRERVFESDRTRFYGAETVSALDYLS 122
Db 93 FPFLVKLEYSFKDNLNLYMVEYVNGGEMFSLHRIGRFSEPHARFYAAQIVLTFEYLHS 152
Qy 123 GKIVYRDLKLENLMDKDGHIKITDFGLCK--EGITDAATMKTFCGTPPEYLAPVLESDND 180
Db 153 LDLIYRDLKPENLIDQGGYIQVTDGFAKRVKGR-----WTLCGTPEYLAPVLESDND 207
Qy 181 YGRAVDWMLGVMYEMMCGRLPFYNQDHEKLFELILMEDIKFPRTLSSDAKSLGILLI 240
Db 208 YNKAVDWWALGVLIYEMAGYPPFPADQPIQIYEKIVSGKVRFPFSSDLKOLLRLNLLQ 267
Qy 241 KDPNKRLLGGGPDDAKEIMRHSFFSGVNMVDYDKLVPPPKPQVTSSETDTRYFDE 295
Db 268 VDLTKRFGNLKGVNDIKNHWKFWATTDWIAIYQKRVKVEAPFIPKFGPGDTSNFDD 322
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RESULT 14
US-11-092-168-4
; Sequence 4, Application US/11092168
; Publication No. US20050277658A1
; GENERAL INFORMATION:
; APPLICANT: Arizona Board of Regents on behalf of The University of Arizona
; APPLICANT: Hurley, Laurence H.
; APPLICANT: Mahadevan, Daruka
; APPLICANT: Han, Haiyong
; APPLICANT: Bears, David J.
; APPLICANT: Vankayalapati, Hariprasad
; APPLICANT: Bashyam, Sridevi
; APPLICANT: Munoz, Ruben M.
; APPLICANT: Warner, Steven L.
; APPLICANT: Della Croce, Kimiko
; APPLICANT: Von Hoff, Daniel D.
; APPLICANT: Grand, Cory L.
; TITLE OF INVENTION: PROTEIN KINASE INHIBITORS
; FILE REFERENCE: 920214.00003CONT3
; CURRENT APPLICATION NUMBER: US/11/092,168
; CURRENT FILING DATE: 2005-03-29
; PRIOR APPLICATION NUMBER: US 10/965,313
; US 60/608,529
; US 60/511,486
; US 60/511,489
; PRIOR FILING DATE: 2004-10-14
; 2004-09-09
; 2003-10-14
; 2003-10-14
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-092-168-4
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Query Match 43.5%; Score 679.5; DB 7; Length 341;
Best Local Similarity 44.4%; Pred. No. 8.7e-52;
Matches 131; Conservative 53; Mismatches 104; Indels 7; Gaps 2;
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Qy 3 MNDPDLKLLGKGTGKGVILVREKASGYAMKILKEVIAKDEVAHTLTESVILKNTNR 62
Db 31 LDQFERIKTLTGSGFGRVLMVKHESGNHYAMKILDKQKVVKLQKQIEHTLNEKRILQAVN 90
Qy 63 HPFLTSLKYSFQTKDRLCFVMEYVNGGELFPHLSRERVFESDRTRFYGAETVSALDYLS 122
Db 91 FPFLVKLEFSFKDNLNLYMVEYVNGGEMFSLHRIGRFAEPHARFYAAQIVLTFEYLHS 150
Qy 123 GKIVYRDLKLENLMDKDGHIKITDFGLCK--EGITDAATMKTFCGTPPEYLAPVLESDND 180
Db 151 LDLIYRDLKPENLIDQGGYIQVTDGFAKRVKGR-----WTLCGTPEYLAPVLESDND 205
Qy 181 YGRAVDWMLGVMYEMMCGRLPFYNQDHEKLFELILMEDIKFPRTLSSDAKSLGILLI 240
Db 206 YNKAVDWWALGVLIYEMAGYPPFPADQPIQIYEKIVSGKVRFPFSSDLKOLLRLNLLQ 265
Qy 241 KDPNKRLLGGGPDDAKEIMRHSFFSGVNMVDYDKLVPPPKPQVTSSETDTRYFDE 295
Db 266 VDLTKRFGNLKGVNDIKNHWKFWATTDWIAIYQKRVKVEAPFIPKFGPGDTSNFDD 320
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RESULT 15
US-11-132-142-14
; Sequence 14, Application US/11132142
; Publication No. US20050276818A1
; GENERAL INFORMATION:
; APPLICANT: The Burnham Institute
; APPLICANT: Sikora, Sergey
; APPLICANT: Godzik, Adam
; TITLE OF INVENTION: UNCHARACTERIZED ORF3 IN SARS-CORONAVIRUS IS A
; FILE REFERENCE: 8014-011-US
; CURRENT APPLICATION NUMBER: US/11/132,142
; CURRENT FILING DATE: 2005-05-17
; PRIOR APPLICATION NUMBER: 60/571,698
; PRIOR FILING DATE: 2004-05-17
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 14
; LENGTH: 351
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-132-142-14
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Best Local Similarity 44.1%; Pred. No. 2e-51;
Matches 130; Conservative 54; Mismatches 104; Indels 7; Gaps 2;
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Qy 3 MNDPDLKLLGKGTGKGVILVREKASGYAMKILKEVIAKDEVAHTLTESVILKNTNR 62
Db 41 LDQFERIKTLTGSGFGRVLMVKHETGNHYAMKILDKQKVVKLQKQIEHTLNEKRILQAVN 100
Qy 63 HPFLTSLKYSFQTKDRLCFVMEYVNGGELFPHLSRERVFESDRTRFYGAETVSALDYLS 122
Db 101 FPFLVKLEFSFKDNLNLYMVEYVNGGEMFSLHRIGRFSEPHARFYAAQIVLTFEYLHS 160
Qy 123 GKIVYRDLKLENLMDKDGHIKITDFGLCK--EGITDAATMKTFCGTPPEYLAPVLESDND 180
Db 161 LDLIYRDLKPENLIDQGGYIQVTDGFAKRVKGR-----WTLCGTPEYLAPVLESDND 215
Qy 181 YGRAVDWMLGVMYEMMCGRLPFYNQDHEKLFELILMEDIKFPRTLSSDAKSLGILLI 240
Db 216 YNKAVDWWALGVLIYEMAGYPPFPADQPIQIYEKIVSGKVRFPFSSDLKOLLRLNLLQ 275
Qy 241 KDPNKRLLGGGPDDAKEIMRHSFFSGVNMVDYDKLVPPPKPQVTSSETDTRYFDE 295
Db 276 VDLTKRFGNLKGVNDIKNHWKFWATTDWIAIYQKRVKVEAPFIPKFGPGDTSNFDD 330
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Job time : 17 secs

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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: February 13, 2006, 06:28:06 ; Search time 309 Seconds  
(without alignments)  
420.894 Million cell updates/sec

Title: US-10-601-311-1\_COPY\_143\_438

Perfect score: 1563

Sequence: 1 KTMNDFYLLKLGKFGKV.....VPPKQVTSDFRYFDEE 296

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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- 1: Geneseqp1980s.\*
- 2: Geneseqp1990s.\*
- 3: Geneseqp2000s.\*
- 4: Geneseqp2001s.\*
- 5: Geneseqp2002s.\*
- 6: Geneseqp2003as.\*
- 7: Geneseqp2003bs.\*
- 8: Geneseqp2004s.\*
- 9: Geneseqp2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1563	100.0	465	3 AAB19011	Aab19011 Amino aci
2	1563	100.0	465	4 AAG78018	Aag78018 Human Act
3	1563	100.0	465	4 AAB19996	Aab19996 Human Ser
4	1563	100.0	465	4 AAB19998	Aab19998 Human Ser
5	1563	100.0	465	8 ADG85255	Adg85255 Human Chr
6	1563	100.0	465	8 ADG85245	Adg85245 Human Chr
7	1563	100.0	479	8 AAB19284	Aab19284 Amino aci
8	1563	100.0	479	3 AAB13393	Aab13393 Human Akt
9	1563	100.0	479	5 AAU79420	Aau79420 Human pro
10	1563	100.0	479	5 ABB06998	Abb06998 Human Akt
11	1563	100.0	479	6 ABR57474	Abt57474 Human PKB
12	1563	100.0	479	7 ADF45034	Adf45034 Human kin
13	1563	100.0	479	8 ADN71940	Adn71940 Human Ser
14	1563	100.0	479	8 ADQ88266	Adq88266 Human 141
15	1558	99.7	454	4 AAG78021	Aag78021 Akt3 rela
16	1555	99.5	479	3 AAB43132	Aab43132 Human ORF
17	1466	93.8	319	4 AAB99833	Aab99833 AGC prote
18	1466	93.8	319	4 ADJ38881	Adj38881 PKBgamma
19	1420.5	90.9	480	8 ADN71942	Adn71942 Chicken s
20	1394.5	89.2	479	2 AAU03453	Aau03453 Mouse c-A
21	1394.5	89.2	480	3 AAY92223	Aay92223 Wild type
22	1394.5	89.2	480	5 AAE17784	Aae17784 Mouse Akt
23	1394.5	89.2	501	2 AAW03452	Aaw03452 Mouse v-A
24	1394.5	89.2	517	8 ADL25357	Adl25357 ARK5 rela

25	1393.5	89.2	480	2 AAW17972	Aaw17972 Human RAC
26	1393.5	89.2	480	2 AAW17984	Aaw17984 Human RAC
27	1393.5	89.2	480	2 AAW18515	Aaw18515 Human AKT
28	1393.5	89.2	480	2 AAY52706	Aay52706 Human AKT
29	1393.5	89.2	480	2 AAY33999	Aay33999 Human AKT
30	1393.5	89.2	480	2 ADF77614	Adf77614 Human Akt
31	1393.5	89.2	480	3 AAY92221	Aay92221 Wild type
32	1393.5	89.2	480	4 AAG78020	Aag78020 Human Akt
33	1393.5	89.2	480	4 AAG67620	Aag67620 Amino aci
34	1393.5	89.2	480	4 AAG67441	Aag67441 Amino aci
35	1393.5	89.2	480	5 AAU79418	Aau79418 Human pro
36	1393.5	89.2	480	5 AAE17782	Aae17782 Human Akt
37	1393.5	89.2	480	5 ABB06996	Abb06996 Human Akt
38	1393.5	89.2	480	6 ABR57472	Abt57472 Human PKB
39	1393.5	89.2	480	7 ADF18630	Adf18630 Human Akt
40	1393.5	89.2	480	7 ADF45032	Adf45032 Human kin
41	1393.5	89.2	480	8 ADL25355	Adl25355 Human ARK
42	1393.5	89.2	480	8 ADO22518	Ado22518 Biochemic
43	1393.5	89.2	480	8 ADQ37844	Adq37844 Human pho
44	1393.5	89.2	480	8 ADR06338	Adr06338 IRK-1 pro
45	1393.5	89.2	480	8 AEM81592	Aem81592 Tumour-as

ALIGNMENTS

RESULT 1  
AAB19011  
ID AAB19011 standard; protein; 465 AA.  
XX AC AAB19011;  
XX DT 08-FEB-2001 (first entry)  
XX DE Amino acid sequence of a human Akt3 polypeptide.  
XX KW Human; Akt3; apoptotic cell death; apoptotic stimulating kinase 1; ASK1;  
KW hypoxia; apoptosis; necrosis; myocardial infarction; ischemia;  
KW reperfusion injury; myocardial ischemia reperfusion injury; stroke;  
KW liver damage; renal failure; organ transplantation; coronary artery.  
XX OS Homo sapiens.  
XX PN WO2000056866-A2.  
XX PD 28-SEP-2000.  
XX PF 14-MAR-2000; 2000WO-US006574.  
XX PR 19-MAR-1999; 99US-0125108P.  
XX PA (AVET ) AVENTIS PHARM PROD INC.  
XX PI Guo K, Pagnoni MF, Clark KL, Ivashchenko YD;  
XX WPI; 2000-638260/61.  
XX DR N-P5DB; AAA96637.  
XX PT Novel AKT3 nucleic acid and proteins capable of preventing apoptotic cell death induced by apoptosis stimulating kinase 1 useful for treating myocardial infarction or ischemia reperfusion injury.  
XX PS Claim 16; Page 64-65; 73pp; English.  
XX CC The present sequence represents a human Akt3 protein. Expression of Akt3 prevents apoptotic cell death induced by apoptotic stimulating kinase 1 (ASK1). The Akt3 polypeptide is useful for inhibiting cell death, preferably in a cardiac myocyte, resulting from hypoxia, apoptosis or necrosis in a patient suffering from myocardial infarction or ischemia reperfusion injury. The polypeptide is also useful for treating myocardial infarction or ischemia reperfusion injury, where the reperfusion injury is myocardial ischemia reperfusion injury or is associated with stroke, liver damage, renal failure, organ

CC transplantation or coronary artery by pass grafting  
XX Sequence 465 AA;  
SQ

Query Match 100.0%; Score 1563; DB 3; Length 465;  
Best Local Similarity 100.0%; Pred. No. 1.1e-155;  
Matches 296; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KTMNDFYLLKLGKGTGKVLVREKASGKYAMKILKKEVIIAKDEVAHTLTESRVLN 60  
Db 143 KTMNDFYLLKLGKGTGKVLVREKASGKYAMKILKKEVIIAKDEVAHTLTESRVLN 202

Qy 61 TRHPFLTSLKYSFQTKDRLCFVMEYVNGGELFFHLSRERFSEDRTRFYGAIEVSALDYL 120  
Db 203 TRHPFLTSLKYSFQTKDRLCFVMEYVNGGELFFHLSRERFSEDRTRFYGAIEVSALDYL 262

Qy 121 HSGKIVYRDLKLENMLDKDGHIKITDFGLCKEGITDAATMKTFCGTPPYLAPEVLEDND 180  
Db 263 HSGKIVYRDLKLENMLDKDGHIKITDFGLCKEGITDAATMKTFCGTPPYLAPEVLEDND 322

Qy 181 YGRAVDWMLGVVMYEMMCGRLPFYNQDHEKLFELILMEDIKFPRTLSSDAKSLLSGLLI 240  
Db 323 YGRAVDWMLGVVMYEMMCGRLPFYNQDHEKLFELILMEDIKFPRTLSSDAKSLLSGLLI 382

Qy 241 KDPNKRLLGGGPDDAKEIMRHSFFSGVNMQDVYDKLVPPFPKQVTSSETDTRYFDEE 296  
Db 383 KDPNKRLLGGGPDDAKEIMRHSFFSGVNMQDVYDKLVPPFPKQVTSSETDTRYFDEE 438

RESULT 2  
AAG78018  
ID AAG78018 standard; protein; 465 AA.  
XX AC AAG78018;  
XX 31-JAN-2002 (first entry)  
XX Human Akt3.  
XX Human; Akt3; AH/PH-domain containing serine/threonine kinase; Akt;  
KW cerebroprotective; neurotropic; hepatotrophic; inhibitor of apoptosis; ASK1;  
KW osteopathic; vasotrophic; neurotrophic; hepatotrophic; inhibitor of apoptosis; ASK1;  
KW apoptosis stimulating kinase 1; hypoxia; necrosis; myocardial infarction;  
KW ischaemia reperfusion injury; stroke; organ transplantation;  
KW coronary artery bypass; tumour cell survival; gene therapy;  
KW Alzheimer's disease; osteoarthritis.  
XX OS Homo sapiens.  
XX WO200168850-A2.  
XX 20-SEP-2001.  
XX 09-MAR-2001; 2001WO-US007663.  
XX 14-MAR-2000; 2000US-00526043.  
XX (AVET ) AVENTIS PHARM PROD INC.  
XX Guo K, Pagnoni MF, Clark KL, Ivashchenko YD;  
XX WPI; 2001-582452/65.  
XX N-PSDB; AAH79025.  
XX New nucleic acid encoding human Akt3 protein, useful for inhibiting cell  
PT death and treating myocardial infarction, ischemia reperfusion injury  
PT associated with stroke, liver damage and renal failure.  
XX Claim 17; Fig 1; 73pp; English.  
XX The invention relates to human Akt3 protein (AH/PH-domain containing  
CC serine/threonine kinase, Akt) comprising a fully defined sequence  
CC (AAG78018) of 465 amino acids, its splice variant or allelic variant,

CC where the encoding polynucleotide hybridises under stringent conditions  
CC with a nucleic acid containing a nucleotide sequence (AAH79025) of 1570  
CC base pairs defined in the specification. Akt3 has cerebroprotective,  
CC neurotropic, hepatotrophic, antiarthritic, osteopathic, vasotrophic and  
CC hepatotrophic activity, as an inhibitor of apoptosis and/or apoptosis  
CC stimulating kinase 1 (ASK1)-induced cell death. Akt3 operably linked to a  
CC regulatory region is useful for inhibiting cell death in cardiac myocytes  
CC resulting from hypoxia, apoptosis or necrosis and for treating myocardial  
CC infarction or ischaemia reperfusion injury, particularly that associated  
CC with stroke, liver damage, renal failure, organ transplantation or  
CC coronary artery bypass grafting. Agonist of Akt3 are useful for improving  
CC Akt3 activity during treatment of patients suffering from myocardial  
CC infarction or ischaemia reperfusion injury and inhibitors of Akt3  
CC activity decrease tumour cell survival and result in tumour regression.  
CC Akt3 protects cells from apoptosis. Gene therapy using Akt3 reduces the  
CC quantity of cell death and final infarct size, resulting in improved post  
CC -infarction function, improved quality of life and reduced mortality. In  
CC patients with existing heart failure, gene therapy with Akt3 retards the  
CC process of ventricular dilation and slows down disease progression. Akt3  
CC gene therapy is useful for treating other disease states, involving cell  
CC death by apoptosis, including Alzheimer's disease, liver degeneration or  
CC osteoarthritis  
XX

Qy 1 KTMNDFYLLKLGKGTGKVLVREKASGKYAMKILKKEVIIAKDEVAHTLTESRVLN 60  
Db 143 KTMNDFYLLKLGKGTGKVLVREKASGKYAMKILKKEVIIAKDEVAHTLTESRVLN 202

Qy 61 TRHPFLTSLKYSFQTKDRLCFVMEYVNGGELFFHLSRERFSEDRTRFYGAIEVSALDYL 120  
Db 203 TRHPFLTSLKYSFQTKDRLCFVMEYVNGGELFFHLSRERFSEDRTRFYGAIEVSALDYL 262

Qy 121 HSGKIVYRDLKLENMLDKDGHIKITDFGLCKEGITDAATMKTFCGTPPYLAPEVLEDND 180  
Db 263 HSGKIVYRDLKLENMLDKDGHIKITDFGLCKEGITDAATMKTFCGTPPYLAPEVLEDND 322

Qy 181 YGRAVDWMLGVVMYEMMCGRLPFYNQDHEKLFELILMEDIKFPRTLSSDAKSLLSGLLI 240  
Db 323 YGRAVDWMLGVVMYEMMCGRLPFYNQDHEKLFELILMEDIKFPRTLSSDAKSLLSGLLI 382

Qy 241 KDPNKRLLGGGPDDAKEIMRHSFFSGVNMQDVYDKLVPPFPKQVTSSETDTRYFDEE 296  
Db 383 KDPNKRLLGGGPDDAKEIMRHSFFSGVNMQDVYDKLVPPFPKQVTSSETDTRYFDEE 438

RESULT 3  
AAB19996  
ID AAB19996 standard; protein; 465 AA.  
XX AC AAB19996;  
XX 28-MAR-2001 (first entry)  
XX Human serine/threonine protein kinase Akt3.  
XX Akt3; human; protein kinase; vascular endothelial growth factor; VEGF;  
KW inducer; ischaemia; cardiomyopathy; angiogenesis; tumour; therapy.  
XX Homo sapiens.  
XX WO2000077190-A2.  
XX 21-DEC-2000.  
XX 01-JUN-2000; 2000WO-US015098.  
XX 11-JUN-1999; 99US-0138724P.  
XX 03-NOV-1999; 99GB-00026058.  
PR

XX (AVET ) AVENTIS PHARM PROD INC.  
PA Guo K, Ivashchenko Y, Clark K;  
XX WPI; 2001-025336/03.  
XX N-PSDB; AAA89264.  
XX Inducing expression of vascular endothelial growth factor, useful for  
PT treating an ischemic condition, e.g. cerebrovascular ischemia, renal  
PT ischemia or pulmonary ischemia, comprises administering a  
PT serine/threonine protein kinase Akt protein.  
XX Example 1; Page 58-59; 67pp; English.  
PS  
XX  
XX The present sequence is that of human Akt3, a novel Akt isoform. Akt3 is  
CC a serine/threonine protein kinase capable of inducing vascular  
CC endothelial growth factor (VEGF) expression. The sequence was deduced  
CC from cDNA (see AAA89264) isolated from a heart cDNA library. Akt3 is  
CC shorter than Akt1 (see AAB19997) and Akt2 (see AAB19998) and there is no  
CC significant homology between Akt3 and Akt1 or Akt2 at the C-terminus of  
CC the molecules. A claimed method of inducing expression of VEGF in a cell  
CC involves administering Akt1, Akt2 or Akt3, or a nucleic acid encoding  
CC such a protein. The cell is preferably from a patient suffering from an  
CC ischaemic condition, especially cerebrovascular, renal, pulmonary, limb  
CC or myocardial ischaemia, or ischaemic, idiopathic or hypertrophic  
CC cardiomyopathy. The result is beneficial collateral blood vessel  
CC formation. A claimed method of inhibiting angiogenesis in a patient  
CC suffering from a tumour, comprises inhibiting the level of Akt activity  
CC in the patient, thereby inhibiting production of VEGF. The method  
CC comprises introducing an Akt antisense nucleic acid, an intracellular  
CC binding protein (e.g. a scfv) that specifically binds the Akt protein, or  
CC a nucleic acid encoding a dominant negative form of an Akt  
XX  
SQ Sequence 465 AA;  
Query Match 100.0%; Score 1563; DB 4; Length 465;  
Best Local Similarity 100.0%; Pred. No. 1.le-155;  
Matches 296; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 KTMNDFYLLKLGKTFGKVLVREKASGYAMKILKKEVIIAKDEVAHTLTESRVLKN 60  
DB 143 KTMNDFYLLKLGKTFGKVLVREKASGYAMKILKKEVIIAKDEVAHTLTESRVLKN 202  
QY 61 TRHPFLTSLKYSFQTKDLRCFVMEYVNGGELFFHLSRERFSEDRTRFYGAIEVSALDYL 120  
DB 203 TRHPFLTSLKYSFQTKDLRCFVMEYVNGGELFFHLSRERFSEDRTRFYGAIEVSALDYL 262  
QY 121 HSGKIVYRDLEMLMDKDGHIKITDFGLCKEGITDAATMKTFCGTPPEYLAPEVLEND 180  
DB 263 HSGKIVYRDLEMLMDKDGHIKITDFGLCKEGITDAATMKTFCGTPPEYLAPEVLEND 322  
QY 181 YGRAVDWGLGVVYEMMCGRLPFYNQDHEKLFELILMEDIKFPRTLSSDAKSLLSGLLI 240  
DB 323 YGRAVDWGLGVVYEMMCGRLPFYNQDHEKLFELILMEDIKFPRTLSSDAKSLLSGLLI 382  
QY 241 KDPNKRLLGGGPDDAKEIMRHSFFSGVNVQDYYDKLVPPFPKQVTSSETDTRFYDSE 296  
DB 383 KDPNKRLLGGGPDDAKEIMRHSFFSGVNVQDYYDKLVPPFPKQVTSSETDTRFYDSE 438  
RESULT 4  
AAB19998  
ID AAB19998 standard; protein; 465 AA.  
XX AAB19998;  
AC  
XX 28-MAR-2001 (first entry)  
DT Human serine/threonine protein kinase Akt2.  
DE  
DE Akt2; human; protein kinase; vascular endothelial growth factor; VEGF;  
KW inducer; ischaemia; cardiomyopathy; angiogenesis; tumour; therapy.

XX Homo sapiens.  
XX WO200077190-A2.  
XX 21-DEC-2000.  
XX 01-JUN-2000; 2000WO-US015098.  
XX 11-JUN-1999; 99US-0138724P.  
XX 03-NOV-1999; 99GB-00026058.  
XX (AVET ) AVENTIS PHARM PROD INC.  
XX Guo K, Ivashchenko Y, Clark K;  
XX WPI; 2001-025336/03.  
XX Inducing expression of vascular endothelial growth factor, useful for  
PT treating an ischemic condition, e.g. cerebrovascular ischemia, renal  
PT ischemia or pulmonary ischemia, comprises administering a  
PT serine/threonine protein kinase Akt protein.  
XX Disclosure; Page 63-64; 67pp; English.  
XX The present sequence is that of human Akt2, a serine/threonine protein  
CC kinase capable of inducing vascular endothelial growth factor (VEGF)  
CC expression. A claimed method of inducing expression of VEGF in a cell  
CC involves administering Akt2, Akt1 (see AAB19997) or Akt3 (see AAB19996),  
CC or a nucleic acid encoding such a protein. The cell is preferably from a  
CC patient suffering from an ischaemic condition, especially  
CC cerebrovascular, renal, pulmonary, limb or myocardial ischaemia, or  
CC ischaemic, idiopathic or hypertrophic cardiomyopathy. The result is  
CC beneficial collateral blood vessel formation. A claimed method of  
CC inhibiting angiogenesis in a patient suffering from a tumour, comprises  
CC inhibiting the level of Akt activity in the patient, thereby inhibiting  
CC production of VEGF. The method comprises introducing an Akt antisense  
CC nucleic acid, an intracellular binding protein (e.g. a scfv) that  
CC specifically binds the Akt protein, or a nucleic acid encoding a dominant  
CC negative form of an Akt  
XX  
SQ Sequence 465 AA;  
Query Match 100.0%; Score 1563; DB 4; Length 465;  
Best Local Similarity 100.0%; Pred. No. 1.le-155;  
Matches 296; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 KTMNDFYLLKLGKTFGKVLVREKASGYAMKILKKEVIIAKDEVAHTLTESRVLKN 60  
DB 143 KTMNDFYLLKLGKTFGKVLVREKASGYAMKILKKEVIIAKDEVAHTLTESRVLKN 202  
QY 61 TRHPFLTSLKYSFQTKDLRCFVMEYVNGGELFFHLSRERFSEDRTRFYGAIEVSALDYL 120  
DB 203 TRHPFLTSLKYSFQTKDLRCFVMEYVNGGELFFHLSRERFSEDRTRFYGAIEVSALDYL 262  
QY 121 HSGKIVYRDLEMLMDKDGHIKITDFGLCKEGITDAATMKTFCGTPPEYLAPEVLEND 180  
DB 263 HSGKIVYRDLEMLMDKDGHIKITDFGLCKEGITDAATMKTFCGTPPEYLAPEVLEND 322  
QY 181 YGRAVDWGLGVVYEMMCGRLPFYNQDHEKLFELILMEDIKFPRTLSSDAKSLLSGLLI 240  
DB 323 YGRAVDWGLGVVYEMMCGRLPFYNQDHEKLFELILMEDIKFPRTLSSDAKSLLSGLLI 382  
QY 241 KDPNKRLLGGGPDDAKEIMRHSFFSGVNVQDYYDKLVPPFPKQVTSSETDTRFYDSE 296  
DB 383 KDPNKRLLGGGPDDAKEIMRHSFFSGVNVQDYYDKLVPPFPKQVTSSETDTRFYDSE 438  
RESULT 5  
ADG85255  
ID ADG85255 standard; protein; 465 AA.  
XX ADG85255;  
AC

XX 25-MAR-2004 (first entry)  
DT Human Chrysoosporium associated protein #3.  
DE  
XX beta-glucosidic bond; beta-xylosidic bond; human.  
XX  
OS Homo sapiens.  
XX US2004002136-A1.  
XX  
XX 01-JAN-2004.  
XX  
XX 21-MAR-2003; 2003US-00394568.  
XX  
XX 06-OCT-1998; 98WO-EP006496.  
PR 06-OCT-1999; 99WO-NL000618.  
PR 13-APR-2000; 2000US-00548938.  
XX

XX (EMAL/) EMALFARB M A.  
PA (BURL/) BURLINGAME R P.  
PA (OLSO/) OLSON P T.  
PA (SINI/) SINITSYN A P.  
PA (PARR/) PARRICHE M.  
PA (BOUS/) BOUSSON J C.  
PA (PYNN/) PYNNONEN C M.  
PA (PUNT/) PUNT P J.  
PA (VZEI/) VAN ZEIJL C M J.  
XX  
PI Emalfarb MA, Burlingame RP, Olson PT, Sinitsyn AP, Parriche M;  
PI Bousson JC, Pynnonen CM, Punt PJ, Van Zeijl CMJ;  
XX  
XX WPI; 2004-061663/06.  
XX  
XX Novel mutant Chrysoosporium strain comprising nucleic acid sequence  
PT encoding polypeptide of interest such as proteases and lipases, the  
PT nucleic acid sequence being operably linked to expression-regulating  
PT region.  
XX  
XX Disclosure; SEQ ID NO 12; 70pp; English.  
XX  
XX The invention relates to a mutant Chrysoosporium strain comprising a  
CC nucleic acid sequence encoding a polypeptide of interest. A mutant  
CC Chrysoosporium strain is useful for producing a polypeptide of interest by  
CC culturing a mutant Chrysoosporium strain under conditions permitting  
CC expression of the protein or polypeptide, and recovering the subsequently  
CC produced polypeptide of interest. The conditions further permit secretion  
CC of the protein or polypeptide of interest. The polypeptides are useful  
CC for hydrolysing beta-glucosidic bonds. A polypeptide is useful for  
CC hydrolysing beta-xylosidic bonds. The present sequence represents a human  
CC Chrysoosporium associated protein.  
XX  
XX Sequence 465 AA;

Query Match 100.0%; Score 1563; DB 8; Length 465;  
Best Local Similarity 100.0%; Pred. No. 1.1e-155;  
Matches 296; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KTNMDFYKLLGLGTFGKVLVREKASGKYAMKILKKEVIAKDEVAHTLTESRVLKN 60  
Db 143 KTNMDFYKLLGLGTFGKVLVREKASGKYAMKILKKEVIAKDEVAHTLTESRVLKN 202  
Qy 61 TRHPFLSLKYSFQTKDRLCFVMEVNGGELFFHLSRERFSEDRTPFYGAIEVSALDYL 120  
Db 203 TRHPFLSLKYSFQTKDRLCFVMEVNGGELFFHLSRERFSEDRTPFYGAIEVSALDYL 262  
Qy 121 HSGKIVYRDLKLEMLDKDGHKIIITDFGLCKEGITDAATMKTCGTPPYLAPEVLEDND 180  
Db 263 HSGKIVYRDLKLEMLDKDGHKIIITDFGLCKEGITDAATMKTCGTPPYLAPEVLEDND 322  
Qy 181 YGRAVDWVGLGVVMEVNGGELFFHLSRERFSEDRTPFYGAIEVSALDYL 240  
Db 323 YGRAVDWVGLGVVMEVNGGELFFHLSRERFSEDRTPFYGAIEVSALDYL 382

Qy 241 KDPNKRLLGGPDDAKKEIMRHSFFSGVNMQDVYDKLVPPFKPQVTSFDTTRYFDEE 296  
Db 383 KDPNKRLLGGPDDAKKEIMRHSFFSGVNMQDVYDKLVPPFKPQVTSFDTTRYFDEE 438

RESULT 6

ADG85245  
ID ADG85245 standard; protein; 465 AA.  
XX  
XX ADG85245;  
AC  
XX 25-MAR-2004 (first entry)  
DT  
XX Human Chrysoosporium associated protein #1.  
DE  
XX beta-glucosidic bond; beta-xylosidic bond; human.  
KW  
XX Homo sapiens.  
OS  
XX US2004002136-A1.  
XX  
XX 01-JAN-2004.  
XX  
XX 21-MAR-2003; 2003US-00394568.  
XX  
XX 06-OCT-1998; 98WO-EP006496.  
PR 06-OCT-1999; 99WO-NL000618.  
PR 13-APR-2000; 2000US-00548938.  
XX

XX (EMAL/) EMALFARB M A.  
PA (BURL/) BURLINGAME R P.  
PA (OLSO/) OLSON P T.  
PA (SINI/) SINITSYN A P.  
PA (PARR/) PARRICHE M.  
PA (BOUS/) BOUSSON J C.  
PA (PYNN/) PYNNONEN C M.  
PA (PUNT/) PUNT P J.  
PA (VZEI/) VAN ZEIJL C M J.  
XX  
XX  
XX Emalfarb MA, Burlingame RP, Olson PT, Sinitsyn AP, Parriche M;  
XX Bousson JC, Pynnonen CM, Punt PJ, Van Zeijl CMJ;  
XX  
XX WPI; 2004-061663/06.  
XX  
XX N-PSDB; ADG85244.  
XX  
XX Novel mutant Chrysoosporium strain comprising nucleic acid sequence  
PT encoding polypeptide of interest such as proteases and lipases, the  
PT nucleic acid sequence being operably linked to expression-regulating  
PT region.  
XX  
XX Disclosure; SEQ ID NO 2; 70pp; English.  
XX

XX The invention relates to a mutant Chrysoosporium strain comprising a  
CC nucleic acid sequence encoding a polypeptide of interest. A mutant  
CC Chrysoosporium strain is useful for producing a polypeptide of interest by  
CC culturing a mutant Chrysoosporium strain under conditions permitting  
CC expression of the protein or polypeptide, and recovering the subsequently  
CC produced polypeptide of interest. The conditions further permit secretion  
CC of the protein or polypeptide of interest. The polypeptides are useful  
CC for hydrolysing beta-glucosidic bonds. A polypeptide is useful for  
CC hydrolysing beta-xylosidic bonds. The present sequence represents a human  
CC Chrysoosporium associated protein.  
XX  
XX Sequence 465 AA;

Query Match 100.0%; Score 1563; DB 8; Length 465;  
Best Local Similarity 100.0%; Pred. No. 1.1e-155;  
Matches 296; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KTNMDFYKLLGLGTFGKVLVREKASGKYAMKILKKEVIAKDEVAHTLTESRVLKN 60  
Db 143 KTNMDFYKLLGLGTFGKVLVREKASGKYAMKILKKEVIAKDEVAHTLTESRVLKN 202

Qy	61	TRHPFLTSLKYSFQTKDRLCFVMEVYVNGGELFFHLSSRVFSEDRTRFFVGABIVSALDYL	120
Db	203	TRHPFLTSLKYSFQTKDRLCFVMEVYVNGGELFFHLSSRVFSEDRTRFFVGABIVSALDYL	262
Qy	121	HSGKIVVRDLKENLMLDKDGHIKITDFGLCKEGITDAATMKTFCGTPPYLAPEVLEND	180
Db	263	HSGKIVVRDLKENLMLDKDGHIKITDFGLCKEGITDAATMKTFCGTPPYLAPEVLEND	322
Qy	181	YGRAVDWMLGVLGVVYEMMCGRLFFYNQDHEKLFELILMEDIKFPRTLSSDAKSLLSGLLI	240
Db	323	YGRAVDWMLGVLGVVYEMMCGRLFFYNQDHEKLFELILMEDIKFPRTLSSDAKSLLSGLLI	382
Qy	241	KDPNKRLLGGGPDDAKEIMRHSPFSFGVNWQDVYDKLVPPFKQVPTSETDTRYPDEE	296
Db	383	KDPNKRLLGGGPDDAKEIMRHSPFSFGVNWQDVYDKLVPPFKQVPTSETDTRYPDEE	438
RESULT	7		
ID	AA19284	standard; protein; 479 AA.	
XX	AA19284;		
DT	19-FEB-2001	(first entry)	
XX		Amino acid sequence of a human kinase B-gamma polypeptide.	
DE		Human; protein kinase B gamma; PKB; insulin; insulin growth factor 1;	
KW		phosphoinositide 3-kinase; insulin signalling;	
KW		pleckstrin homology domain.	
XX			
OS		Homo sapiens.	
XX			
FH		Key Location/Qualifiers	
FT		Modified-site 305	
FT		/note= "active phosphorylation site"	
FT		Modified-site 472	
FT		/note= "putative phosphorylation site"	
XX			
PN		WO200058446-A1.	
XX			
PD		05-OCT-2000.	
XX			
PF		23-MAR-2000; 2000WO-SE000571.	
XX			
PR		25-MAR-1999; 99SE-00001115.	
XX			
PA		(PHAA ) PHARMACIA & UPJOHN AB.	
XX			
PI		Attersand A;	
XX			
DR		WPI; 2000-647230/62.	
XX		N-PSDB; AAC61592.	
XX			
PT		Novel human protein kinase B gamma polynucleotides and polypeptides	
PT		useful as probe or primers in polymerase chain reaction and to raise	
PT		antibodies useful in diagnostic assays for detecting polypeptide	
XX		expression.	
XX			
PS		Claim 8; Page 19-20; 27pp; English.	
XX			
CC		The present sequence represents a human protein kinase B gamma (PKB)	
CC		polypeptide. PKB is activated by insulin or insulin growth factor 1.	
CC		Lipid products of phosphoinositide 3-kinase act in insulin signalling by	
CC		binding to pleckstrin homology domains of PKB. PKB polynucleotides may be	
CC		used as a source of probes and primers. PKB polypeptides are used to	
CC		raise antibodies, which are used in diagnostic assays. The polypeptides	
CC		are also useful for screening for compounds which affect insulin	
CC		signalling pathways	
XX			
SQ		Sequence 479 AA;	

CC	matrix. The Akt-3 nucleic acid molecule and protein may be used as
CC	medications for treating cancer. Agents which influence the activity of
CC	Akt-3 protein, and so stimulate apoptosis, may also be used to treat
CC	diseases associated with Akt-3
XX	
SQ	Sequence 479 AA;
	Query Match 100.0%; Score 1563; DB 3; Length 479;
	Best Local Similarity 100.0%; Pred. No. 1.2e-155;
	Matches 296; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	1 KTWNDFYLLKLGKTGKVILVREKASGYAMKILKKEVIIAKDEVAHTLTESRVLN 60
Dd	143 KTWNDFYLLKLGKTGKVILVREKASGYAMKILKKEVIIAKDEVAHTLTESRVLN 202
Qy	61 TRHPFLTSLKYSPOTKDRLCFVMIEYVNGGELFPHLSRVPSEDRTFYGAIEVSALDYL 120
Dd	203 TRHPFLTSLKYSPOTKDRLCFVMIEYVNGGELFPHLSRVPSEDRTFYGAIEVSALDYL 262
Qy	121 HSGKIVVRDLKLENMLDKOGHIIKITDFGLCKEGITDAATMKTCGTPYIAPLVELEND 180
Dd	263 HSGKIVVRDLKLENMLDKOGHIIKITDFGLCKEGITDAATMKTCGTPYIAPLVELEND 322
Qy	181 YGRAVDWNLGVNVYEMMCGRLPFYNODHEKLFELLIMEDIKFPTLTSSDAKSLLSGLLI 240
Dd	323 YGRAVDWNLGVNVYEMMCGRLPFYNQDHEKLFELLIMEDIKFPTLTSSDAKSLLSGLLI 382
Qy	241 KDPNKRLGGGPDDAKEIMRHSFFFSGVNQDVYDKLVPPFPKQVTSSTDTRYFDEE 296
Dd	383 KDPNKRLGGGPDDAKEIMRHSFFFSGVNQDVYDKLVPPFPKQVTSSTDTRYFDEE 438

RESULT 9	
AAU79420	
ID	AAU79420 standard; protein; 479 AA.
XX	
AC	AAU79420;
XX	
XX	
DT	02-JUL-2002 (first entry)
XX	
XX	Human protein kinase B gamma.
XX	
XX	Human; integrin-linked kinase; ILK; presenilin-1; protein kinase B; PKB;
KW	gamma secretase; apoptosis; Alzheimer's disease; PS-1; neurotropic;
KW	neuroprotective; cytostatic; cancer.
XX	
OS	Homo sapiens.
XX	
XX	WO200222862-A2.
PN	
XX	
PD	21-MAR-2002.
XX	
XX	
PF	12-SEP-2001; 2001WO-GB004094.
XX	
PR	12-SEP-2000; 2000GB-00022333.
XX	
PA	(GLAX ) GLAXO GROUP LTD.
XX	
PI	Hiles ID, Ellis C;
XX	
DR	WPI; 2002-351896/38.
XX	
PT	Identifying agent that modulates interaction between integrin-linked
PT	kinase and presenilin-1, useful for treating Alzheimer's disease, and
PT	identifying agent that modulates protein kinase B or gamma secretase
PT	activity.
XX	
PS	Disclosure; Page 50-52; 53pp; English.
XX	
CC	The invention relates to identifying an agent modulating interaction
CC	between integrin-linked kinase (ILK) and presenilin-1 (PS1) comprising
CC	providing ILK, PS1 or their functional variants, as first and second
CC	components respectively, contacting the components in the presence of a

CC	test agent under conditions that in absence of the agent, would permit
CC	the components to interact and determining whether the agent is capable
CC	of modulating the interaction between the components. Also included are
CC	the method above where the components are protein kinase beta (PKB),
CC	gamma secretase or their functional variants, test kits for carrying out
CC	the methods and an agent identified by the methods. The methods are used
CC	for identifying an agent that modulates interaction between ILK and PSI.
CC	or PKB or gamma-secretase. The agent has therapeutic applications in
CC	treating humans or animals, for treating a host suffering from a
CC	condition associated with an interaction between ILK and PSI. activity of
CC	PKB, activity of gamma-secretase, apoptosis, cancer and Alzheimer's
CC	disease. The agent is also useful for manufacturing a medicament for use
CC	in treatment of the above mentioned conditions. The present sequence
XX	represents human protein kinase B gamba
XX	
SQ	Sequence 479 AA;
	Query Match 100.0%; Score 1563; DB 5; Length 479;
	Best Local Similarity 100.0%; Pred. No. 1.2e-155;
	Matches 296; Conservative 0; Mismatches 0; Indels 0; Gaps 0
Qy	1 KTNMDFYLKLGLGTFGKVTLVREKASGKYAMKILKEVIIAKDEVAHTLTESRVLKN 60
Db	143 KTNMDFYLKLGLGTFGKVTLVREKASGKYAMKILKEVIIAKDEVAHTLTESRVLKN 202
Qy	61 TRHPFLTSLKYSFQTQRCLCFWMEYVNGGELFFHLSSRRVFSEDRTRFYGAIVSALDYL 120
Db	203 TRHFFLTSLKYSFQTQRCLCFWMEYVNGGELFFHLSSRRVFSEDRTRFYGAIVSALDYL 262
Qy	121 HSGKIVYRDCLKENLMLDKGHHKITDPGLCKEGITDAATWKTCGTPEYLAPEVLND 180
Db	263 HSGKIVYRDCLKENLMLDKGHHKITDPGLCKEGITDAATWKTCGTPEYLAPEVLND 322
Qy	181 YGRAVDWMGLGVVMYEMWCGRLPFYNQDHXL FELILMEDIKFPETLSSDAKSLLSGLLI 240
Db	323 YGRAVDWMGLGVVMYEMWCGRLPFYNQDHXL FELILMEDIKFPETLSSDAKSLLSGLLI 382
Qy	241 KDPNKRLOGGGDDAKEIMRHSFFFGVNWDVKLVPPFKPQVTSETDTRYFDEE 296
Db	383 KDPNKRLOGGGDDAKEIMRHSFFFGVNWDVKLVPPFKPQVTSETDTRYFDEE 438
RESULT 10	
ABB06998	
ID	ABB06998 standard; protein; 479 AA.
AC	ABB06998;
XX	
DT	20-JUN-2002 (first entry)
XX	
DE	Human Akt3 protein SEQ ID NO:9.
XX	
KW	Human; Hsp90 beta; Hsp90 alpha; Akt1; Akt2; Akt3; apoptosis regulation;
KW	apoptosis; serine/threonine kinase; heat shock protein; anticancer;
KW	cycostatic; cardiant; vasotropic; hepatotropic; neuroprotective;
KW	anti-diabetic; nootropic; cancer; diabetes; Alzheimer's disease;
KW	cell death; radiation; brain ischaemia; cardiac ischaemia.
OS	Homo sapiens.
XX	
FN	WO200215925-A1.
XX	
PD	28-FEB-2002.
XX	
PF	22-AUG-2001; 2001WO-JP007179.
XX	
PR	22-AUG-2000; 2000JP-00251529.
XX	
PA	(KYOW ) KYOWA HAKKO KOGYO KK.
FA	(TSUR/) TSURUO T.
PI	Tsuruo T, Fujita N, Sato S;

DR WPI: 2002-292035/33.  
DR N-PSDB; ABL50839.  
XX  
PT Regulation of apoptosis by promoting or inhibiting the intracellular  
PT binding of Akt with Hsp90, useful for prevention and treatment of  
PT apoptosis-regulation associated diseases including cancer.  
XX  
PS Claim 12; Page 85-87; 93pp; Japanese.  
XX  
CC The present invention describes the regulation of apoptosis, in which the  
CC intracellular binding of Akt (a serine/threonine kinase) with Hsp90 (a  
CC heat-shock protein) is promoted or inhibited. The present invention also  
CC describes: (1) isoforms of Akt and Hsp90, and their partial peptides  
CC including the binding domain; (2) antibodies to Akt or Hsp90; (3) DNA  
CC encoding Akt or Hsp90 or their partial peptides including the binding  
CC domain; (4) expression vectors containing the DNA; (5) host cells  
CC transformed by the vectors; (6) production of Akt or Hsp90 or their  
CC partial peptides including the binding domain by culture of the  
CC transformed cells; (7) screening compounds for their ability to modify  
CC intracellular Akt activity by contact with cells expressing Akt or Hsp90;  
CC and (8) drug compositions containing antibodies recognizing the binding  
CC domain of Akt or Hsp90 and optionally also an anticancer agent. Akt and  
CC Hsp90 have cytostatic, cardiant, vasotropic, hepatotropic, antidiabetic,  
CC neuroprotective and neurotropic activities. Blockade of the binding of  
CC Hsp90 with Akt increases the sensitivity of cells to apoptosis induction.  
CC Akt and Hsp90 can be used in the prevention and treatment of diseases  
CC with which apoptosis regulation is associated, including cancer (such as  
CC gastric cancer, ovarian cancer, breast cancer, pancreatic cancer and  
CC prostate cancer), diabetes, Alzheimer's disease, cell death caused by  
CC radiation or anticancer agents, brain ischaemia or cardiac ischaemia. The  
CC present sequence represents human Akt3 which is used in the  
CC exemplification of the present invention  
XX  
SQ Sequence 479 AA;  
  
Query Match 100.0%; Score 1563; DB 5; Length 479;  
Best Local Similarity 100.0%; Pred. No. 1.2e-155;  
Matches 296; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 KTMNDFYLLKLGKGTGKGVILVREKASGKYAMKILKEVIIAKDEVAHTLTESRVLKN 60  
DB 143 KTMNDFYLLKLGKGTGKGVILVREKASGKYAMKILKEVIIAKDEVAHTLTESRVLKN 202  
  
QY 61 TRHPFLTSLKYSFQTKDRLCFVMEYVNGGELFFHLSRERVSFSEDRTRFYGABIVSALDYL 120  
DB 203 TRHPFLTSLKYSFQTKDRLCFVMEYVNGGELFFHLSRERVSFSEDRTRFYGABIVSALDYL 262  
  
QY 121 HSGKIVYRDLKLENLMLDKDGHIKITDFGLCKEGITDAATMTKTCGTPPYLAPEVLEND 180  
DB 263 HSGKIVYRDLKLENLMLDKDGHIKITDFGLCKEGITDAATMTKTCGTPPYLAPEVLEND 322  
  
QY 181 YGRAVDWVGLGVVYEMMCGRLPFYVQNDHEKLFELILMEDIKFPRTLSSDAKSLSGLLI 240  
DB 323 YGRAVDWVGLGVVYEMMCGRLPFYVQNDHEKLFELILMEDIKFPRTLSSDAKSLSGLLI 382  
  
QY 241 KDPNKRLLGGPDDAKEIMRHSFFSGVNWQDVYDKLVPPFPKQVTSSETDTRYFDEE 296  
DB 383 KDPNKRLLGGPDDAKEIMRHSFFSGVNWQDVYDKLVPPFPKQVTSSETDTRYFDEE 438  
  
RESULT 11  
ABR57474  
ID ABR57474 standard; protein; 479 AA.  
XX  
AC ABR57474;  
XX  
DT 15-SEP-2003 (first entry)  
DE Human PKB-gamma amino acid sequence.  
XX  
KW Protein kinase B; PKB/Akt; enzyme; crystal structure; drug discovery;  
KW protein co-ordinate data; cytostatic; antidiabetic; vasotropic; PKB;  
KW neurotropic; neuroprotective; gene therapy; protein kinase B beta; PKBbeta;

KW structural analysis; cancer; diabetes; erectile dysfunction; human;  
KW neurodegeneration.  
XX  
OS Homo sapiens.  
XX  
PN WO2003016516-A2.  
XX  
PD 27-FEB-2003.  
XX  
PF 14-AUG-2002; 2002WO-GB003735.  
XX  
PR 14-AUG-2001; 2001GB-00019860.  
PR 01-MAY-2002; 2002GB-00009985.  
XX  
PA (NOVS ) NOVARTIS FORSCHUNGSSTIFTUNG ZWEIGNIEDERL.  
PA (CANC-) CANCER RES INST.  
XX  
PI Barford D, Yang J, Hemmings BA, Cron PD;  
XX WPI; 2003-268328/26.  
DR New crystal of protein kinase B beta, useful for activating protein  
XX kinases, e.g. AGC kinases, comprises three-dimensional atomic coordinates  
PT of a tetragonal space group.  
PT Disclosure; Fig 7; 284pp; English.  
PS  
XX The present invention describes a crystal of protein kinase B beta  
CC (PKBbeta) comprising (I), where (I) comprises: (a) a tetragonal space  
CC group P4-1-2-1-2 and unit cell dimensions of: a = 149.33 plus or minus  
CC 0.5 Angstrom, b = 149.33 plus or minus 0.5 Angstrom, c = 39.77 plus or  
CC minus 0.5 Angstrom; a = 148.40 plus or minus 0.5 Angstrom, b = 148.40  
CC plus or minus 0.5 Angstrom, c = 38.55 plus or minus 0.5 Angstrom; a =  
CC 149.70 plus or minus 0.5 Angstrom, b = 149.70 plus or minus 0.5 Angstrom, c = 39.19  
CC plus or minus 0.5 Angstrom; or a = 149.52 plus or minus 0.5 Angstrom, b = 149.52  
CC plus or minus 0.5 Angstrom, c = 39.06 plus or minus 0.5 Angstrom, or  
CC 0.5 Angstrom; or (b) the three-dimensional atomic coordinates listed in  
CC the specification. (I) has cytostatic, antidiabetic, vasotropic,  
CC neurotropic and neuroprotective activities, and can be used in gene  
CC therapy. The crystal of PKBbeta, and methods from the present invention,  
CC are useful in activating protein kinases, particularly AGC kinases, for  
CC identifying modulators of protein kinase activity, and for structural  
CC analysis of other protein kinases. The crystal may also be used in  
CC manufacturing a medicament for treating cancers, diabetes, erectile  
CC dysfunction or neurodegeneration. The present sequence represents the  
CC human PKB-gamma amino acid sequence, which is given in the  
CC exemplification of the present invention  
XX  
SQ Sequence 479 AA;  
  
Query Match 100.0%; Score 1563; DB 6; Length 479;  
Best Local Similarity 100.0%; Pred. No. 1.2e-155;  
Matches 296; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 KTMNDFYLLKLGKGTGKGVILVREKASGKYAMKILKEVIIAKDEVAHTLTESRVLKN 60  
DB 143 KTMNDFYLLKLGKGTGKGVILVREKASGKYAMKILKEVIIAKDEVAHTLTESRVLKN 202  
  
QY 61 TRHPFLTSLKYSFQTKDRLCFVMEYVNGGELFFHLSRERVSFSEDRTRFYGABIVSALDYL 120  
DB 203 TRHPFLTSLKYSFQTKDRLCFVMEYVNGGELFFHLSRERVSFSEDRTRFYGABIVSALDYL 262  
  
QY 121 HSGKIVYRDLKLENLMLDKDGHIKITDFGLCKEGITDAATMTKTCGTPPYLAPEVLEND 180  
DB 263 HSGKIVYRDLKLENLMLDKDGHIKITDFGLCKEGITDAATMTKTCGTPPYLAPEVLEND 322  
  
QY 181 YGRAVDWVGLGVVYEMMCGRLPFYVQNDHEKLFELILMEDIKFPRTLSSDAKSLSGLLI 240  
DB 323 YGRAVDWVGLGVVYEMMCGRLPFYVQNDHEKLFELILMEDIKFPRTLSSDAKSLSGLLI 382  
  
QY 241 KDPNKRLLGGPDDAKEIMRHSFFSGVNWQDVYDKLVPPFPKQVTSSETDTRYFDEE 296  
DB 383 KDPNKRLLGGPDDAKEIMRHSFFSGVNWQDVYDKLVPPFPKQVTSSETDTRYFDEE 438

RESULT 12  
ADF45034  
ID ADF45034 standard; protein; 479 AA.  
XX  
AC ADF45034;  
XX  
DT 12-FEB-2004 (first entry)  
XX  
DE Human kinase AKT3.  
XX  
KW Human; protein kinase; enzyme; inhibitor; AKT3.  
XX  
OS Homo sapiens.  
XX  
PN WO2003081210-A2.  
XX  
PD 02-OCT-2003.  
XX  
PF 20-MAR-2003; 2003WO-US008725.  
XX  
PR 21-MAR-2002; 2002US-0366892P.  
XX  
PA (SUNE-) SUNESIS PHARM INC.  
XX  
PI Prescott JC, Braisted A;  
XX  
XX WPI; 2003-865136/80.  
XX  
XX Identifying ligand binding to inactive conformation of target protein kinase (T) comprises contacting the conformation modified (T) which contains reactive group at binding site, with ligands and detecting kinase-ligand conjugate formation.  
XX  
PS Disclosure; SEQ ID NO 3; 260pp; English.  
XX  
XX The present invention relates to a method for identifying a ligand (L), which binds to an inactive conformation of target protein kinase (T). The method involves contacting inactive conformation of (T), which contains or is modified to contain a reactive group at or near a binding site of interest, with one or more ligand candidates capable of covalently bonding to the reactive group thus forming a kinase-(L) conjugate (C). The method is useful for identifying protein kinase inhibitors that preferentially bind to inactive conformation of a target protein kinase. The present sequence is a protein kinase which may be modified via an amino acid substitution, for use in the method of the invention.  
XX  
SQ Sequence 479 AA;  
Query Match 100.0%; Score 1563; DB 7; Length 479;  
Best Local Similarity 100.0%; Pred. No. 1.2e-155;  
Matches 296; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 KTMNDFYLLKLGKGTGKVLVREKASGKYAMKILKKEVIAAKDEVAHTLTESRVLKN 60  
Db 143 KTMNDFYLLKLGKGTGKVLVREKASGKYAMKILKKEVIAAKDEVAHTLTESRVLKN 202  
Qy 61 TRHPFLTSLKYSFQTKORLCFVMEYVNGGELFFHLSRERFSEDRTPFYGAIVSALDYL 120  
Db 203 TRHPFLTSLKYSFQTKORLCFVMEYVNGGELFFHLSRERFSEDRTPFYGAIVSALDYL 262  
Qy 121 HSGKIVYRDLKLENLMDKDGHKITDFTGLCKEGITDAATMKTFCTGPEYLAPVLEND 180  
Db 263 HSGKIVYRDLKLENLMDKDGHKITDFTGLCKEGITDAATMKTFCTGPEYLAPVLEND 322  
Qy 181 YGRAVDWVGLGVVMEYVNGGELFFHLSRERFSEDRTPFYGAIVSALDYL 240  
Db 323 YGRAVDWVGLGVVMEYVNGGELFFHLSRERFSEDRTPFYGAIVSALDYL 382  
Qy 241 KDPNKRLLGGGPDDAKEIMRHSFFSGVNWQDYVDKLVPPFPQVTSQTDTRYFDEE 296  
Db 383 KDPNKRLLGGGPDDAKEIMRHSFFSGVNWQDYVDKLVPPFPQVTSQTDTRYFDEE 438

RESULT 13  
ADN71940  
ID ADN71940 standard; protein; 479 AA.  
XX  
AC ADN71940;  
XX  
DT 12-AUG-2004 (first entry)  
XX  
DE Human serine/threonine kinase Akt-3 protein SEQ ID NO:26.  
XX  
KW kinase pathway inhibitor; anti-prostate cancer;  
KW mitogen-activated protein kinase pathway inhibitor;  
KW MAP kinase pathway inhibitor; prostate cancer inhibitor;  
KW phosphatidylinositol 3-kinase/Akt kinase pathway;  
KW PI3K/Akt kinase pathway; cytoskeletal; MAP kinase inhibitor;  
KW phosphatidylinositol 3-kinase/Akt kinase inhibitor;  
KW PI3K/Akt kinase inhibitor; androgen receptor inhibitor; prostate cancer;  
KW human; serine/threonine kinase Akt-3; chromosome 1.  
XX  
OS Homo sapiens.  
XX  
PN WO2004041185-A2.  
XX  
PD 21-MAY-2004.  
XX  
PF 31-OCT-2003; 2003WO-US034636.  
XX  
PR 31-OCT-2002; 2002US-0423340P.  
XX  
PA (UYRP ) UNIV ROCHESTER.  
XX  
PI Chang C, Lee Y, Lin W;  
XX  
XX WPI; 2004-390508/36.  
XX  
DR N-PSDB; ADN71939.  
XX  
XX Composition useful in the treatment of e.g. prostate cancer comprises a kinase pathway inhibitor and an anti-prostate cancer compound.  
XX  
PS Disclosure; SEQ ID NO 26; 118pp; English.  
XX  
XX The present invention describes a composition (C1) which comprises a kinase pathway inhibitor (a) and an anti-prostate cancer compound (b). Also described: (1) identification of a mitogen-activated protein (MAP) kinase pathway inhibitor involving incubating an antiandrogen or a library of molecules with a cell containing an activable MAP kinase pathway and selecting the molecules which inhibit the activation of the MAP kinase pathway; and (2) identification of a prostate cancer inhibitor involving incubating a cell with hydroxyflutamide and potential inhibitor, and assaying the level of activation of MAP kinase pathway or phosphatidylinositol 3-kinase (PI3K)/Akt kinase pathway. C1 has cytostatic activity, and can be used as a MAP kinase inhibitor, phosphatidylinositol 3-kinase (PI3K)/Akt kinase inhibitor, and androgen receptor (AR) inhibitor. C1 can be used in the treatment of prostate cancer; for identifying a MAP kinase pathway inhibitor; for identifying a prostate cancer inhibitor; and for reducing the number of prostate cancer cells in a sample. The composition C1 provides effective combination therapy as compared to prior therapies. The present sequence represents human serine/threonine kinase Akt-3, which is used in the exemplification of the present invention.  
XX  
SQ Sequence 479 AA;  
Query Match 100.0%; Score 1563; DB 8; Length 479;  
Best Local Similarity 100.0%; Pred. No. 1.2e-155;  
Matches 296; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 KTMNDFYLLKLGKGTGKVLVREKASGKYAMKILKKEVIAAKDEVAHTLTESRVLKN 60  
Db 143 KTMNDFYLLKLGKGTGKVLVREKASGKYAMKILKKEVIAAKDEVAHTLTESRVLKN 202



QY 61 TRHPFLTSKYSFQTKDRLCFVMEYVNGGELFFHLSSRVFSEDRTRFYGAIVSALDYL 120  
Db 203 TRHPFLTSKYSFQTKDRLCFVMEYVNGGELFFHLSSRVFSEDRTRFYGAIVSALDYL 262  
QY 121 HSGKIVYRDLKLENMLDKDGHIKITDFGLCKEGITDAATMTKTFCTPEYLAPEVLEND 180  
Db 263 HSGKIVYRDLKLENMLDKDGHIKITDFGLCKEGITDAATMTKTFCTPEYLAPEVLEND 322  
QY 181 YGRAVDWVWGLGVVYEMMCGRLPFFYNQDHEKLFELILMEDIKFPRTLSDDAKSLLSGLLI 240  
Db 323 YGRAVDWVWGLGVVYEMMCGRLPFFYNQDHEKLFELILMEDIKFPRTLSDDAKSLLSGLLI 382  
QY 241 KDPNKRLLGGGPDDAKEIMRHSFFSGVNWQDVYDKLVPPFKPQVTSSETDTRFYDEE 296  
Db 393 KDPNKRLLGGGPDDAKEIMRHSFFSGVNWQDVYDKLVPPFKPQVTSSETDTRFYDEE 438  
RESULT 14  
ADQ88266  
ID ADQ88266 standard; protein; 479 AA.  
AC ADQ88266;  
XX  
DT 21-OCT-2004 (first entry)  
XX  
DE Human 14180 protein, a rac gamma Ser/Thr protein kinase RAC-PK-gamma.  
XX  
KW human; cardiovascular disorder; thrombotic disorder;  
KW differential expression; gene therapy; aberrant vascularisation;  
KW atherosclerosis; thrombosis; coronary artery disease; hyperlipidaemia;  
KW dyslipidaemia; high blood pressure; heart failure; cardiand;  
KW thrombolytic; anticoagulant; antilipemic; hypotensive; cardiand;  
KW rac gamma Ser/Thr protein kinase; RAC-PK-gamma; EC 2.7.1.-; enzyme.  
XX  
OS Homo sapiens.  
XX  
XX WO2004063340-A2.  
XX  
PD 29-JUL-2004.  
XX  
XX  
PF 13-JAN-2004; 2004WO-US000393.  
XX  
PR 13-JAN-2003; 2003US-0439683P.  
PR 05-FEB-2003; 2003US-0445216P.  
PR 18-FEB-2003; 2003US-0448036P.  
PR 12-MAR-2003; 2003US-0454189P.  
PR 25-MAR-2003; 2003US-0457541P.  
PR 29-APR-2003; 2003US-0466411P.  
PR 08-MAY-2003; 2003US-0469041P.  
PR 10-JUN-2003; 2003US-0477414P.  
PR 13-JUN-2003; 2003US-0478560P.  
PR 24-JUL-2003; 2003US-0489772P.  
PR 28-JUL-2003; 2003US-0490660P.  
PR 03-SEP-2003; 2003US-0499838P.  
PR 22-SEP-2003; 2003US-0504788P.  
PR 24-SEP-2003; 2003US-0505570P.  
PR 17-OCT-2003; 2003US-0512418P.  
PR 27-OCT-2003; 2003US-0514660P.  
XX (MILL-) MILLENNIUM PHARM INC.  
XX  
XX Stagliano NE, Healy A, Acton SL, Galvin KM, Donoghue MA;  
PI Rogrigue-Way A, Tomlinson JE;  
XX  
XX WPI: 2004-553729/53.  
DR N-PSDB; ADQ88265.  
XX  
XX Identifying a compound for treating a cardiovascular or thrombotic  
PT disorder by combining a compound to be tested with e.g., a 9380, 9462,  
PT 8701 or 2419 polypeptide or with a host cell expressing the polypeptide  
PT and detecting the binding.  
XX  
PS Claim 1; SEQ ID NO 108; 512pp; English.

XX This invention relates to a novel compound that is capable of treating a  
CC cardiovascular or thrombotic disorder. Specifically, it refers to the  
CC identification of nucleic acid molecules, and the encoded proteins  
CC thereof, which are differentially expressed in cardiovascular disease  
CC states relative to their normal expression in non-diseased tissue. The  
CC present invention describes test compounds (i.e. small molecules,  
CC peptides or antibodies) that can bind to and modulate the activity of  
CC these differentially expressed membrane-bound polypeptides, where binding  
CC is detected by a competition binding assay, immunoassay or yeast two-  
CC hybrid assay. Accordingly, pharmaceutical compositions can be developed  
CC and used via gene therapy to treat aberrant vascularisation.  
CC atherosclerosis, thrombosis, coronary artery disease, hyperlipidaemia,  
CC dyslipidaemia, high blood pressure or heart failure. As such, they  
CC exhibit cardiand, thrombolytic, anticoagulant, antilipemic, hypotensive  
CC and cardiand activities. This polypeptide sequence is a human protein  
CC that is differentially expressed in a patient with a cardiovascular  
CC disorder, given in an exemplification of the invention.  
XX  
SQ Sequence 479 AA;  
Query Match 100.0%; Score 1563; DB 8; Length 479;  
Best Local Similarity 100.0%; Pred. No. 1.2e-155;  
Matches 296; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 KTMNDFVYLKLGKGTGKVLVREKASGKYVAMKILKKEVIIAKDEVAHTLTESRVLKN 60  
Db 143 KTMNDFVYLKLGKGTGKVLVREKASGKYVAMKILKKEVIIAKDEVAHTLTESRVLKN 202  
QY 61 TRHPFLTSKYSFQTKDRLCFVMEYVNGGELFFHLSSRVFSEDRTRFYGAIVSALDYL 120  
Db 203 TRHPFLTSKYSFQTKDRLCFVMEYVNGGELFFHLSSRVFSEDRTRFYGAIVSALDYL 262  
QY 121 HSGKIVYRDLKLENMLDKDGHIKITDFGLCKEGITDAATMTKTFCTPEYLAPEVLEND 180  
Db 263 HSGKIVYRDLKLENMLDKDGHIKITDFGLCKEGITDAATMTKTFCTPEYLAPEVLEND 322  
QY 181 YGRAVDWVWGLGVVYEMMCGRLPFFYNQDHEKLFELILMEDIKFPRTLSDDAKSLLSGLLI 240  
Db 323 YGRAVDWVWGLGVVYEMMCGRLPFFYNQDHEKLFELILMEDIKFPRTLSDDAKSLLSGLLI 382  
QY 241 KDPNKRLLGGGPDDAKEIMRHSFFSGVNWQDVYDKLVPPFKPQVTSSETDTRFYDEE 296  
Db 393 KDPNKRLLGGGPDDAKEIMRHSFFSGVNWQDVYDKLVPPFKPQVTSSETDTRFYDEE 438  
RESULT 15  
AAG78021  
ID AAG78021 standard; protein; 454 AA.  
XX  
AC AAG78021;  
XX  
DT 31-JAN-2002 (first entry)  
XX  
DE Akt3 related polypeptide.  
XX  
KW Human; Akt3; AH/PH-domain containing serine/threonine kinase; Akt;  
KW cerebroprotective; neurotropic; neuroprotective; antiarthritic;  
KW osteopathic; vasotropic; hepatotrophic; inhibitor of apoptosis; ASK1;  
KW apoptosis stimulating kinase 1; hypoxia; necrosis; myocardial infarction;  
KW ischaemia reperfusion injury; stroke; organ transplantation;  
KW coronary artery bypass; tumour cell survival; gene therapy;  
KW Alzheimer's disease; osteoarthritis.  
XX  
OS Unidentified.  
XX  
XX WO200168850-A2.  
XX  
PD 20-SEP-2001.  
XX  
XX 09-MAR-2001; 2001WO-US007663.  
XX  
XX 14-MAR-2000; 2000US-00526043.  
PR

XX (AVET ) AVENTIS PHARM PROD INC.  
XX  
XX Guo K, Pagnoni MF, Clark KL, Ivashchenko YD;  
XX  
XX WPI; 2001-582452/65.  
XX  
XX New nucleic acid encoding human Akt3 protein, useful for inhibiting cell  
PT death and treating myocardial infarction, ischemia reperfusion injury  
PT associated with stroke, liver damage and renal failure.  
XX  
XX Disclosure; Page 72-73; 73pp; English.  
XX  
XX The invention relates to human Akt3 protein (AH/PH-domain containing  
CC serine/threonine kinase, Akt) comprising a fully defined sequence  
CC (AAG78018) of 465 amino acids, its splice variant or allelic variant,  
CC where the encoding polynucleotide hybridises under stringent conditions  
CC with a nucleic acid containing a nucleotide sequence (AAH79025) of 1570  
CC base pairs defined in the specification. Akt3 has cerebroprotective,  
CC neurotrophic, neuroprotective, antiarthritic, osteopathic, vasotropic and  
CC hepatotrophic activity, as an inhibitor of apoptosis and/or apoptosis  
CC stimulating kinase 1 (ASK1)-induced cell death. Akt3 operably linked to a  
CC regulatory region is useful for inhibiting cell death in cardiac myocytes  
CC resulting from hypoxia, apoptosis or necrosis and for treating myocardial  
CC infarction or ischaemia reperfusion injury, particularly that associated  
CC with stroke, liver damage, renal failure, organ transplantation or  
CC coronary artery bypass grafting. Agonist of Akt3 are useful for improving  
CC Akt3 activity during treatment of patients suffering from myocardial  
CC infarction or ischaemia reperfusion injury and inhibitors of Akt3  
CC activity decrease tumour cell survival and result in tumour regression.  
CC Akt3 protects cells from apoptosis. Gene therapy using Akt3 reduces the  
CC quantity of cell death and final infarct size, resulting in improved post  
CC -infarction function, improved quality of life and reduced mortality. In  
CC patients with existing heart failure, gene therapy with Akt3 retards the  
CC process of ventricular dilation and slows down disease progression. Akt3  
CC gene therapy is useful for treating other disease states, involving cell  
CC death by apoptosis, including Alzheimer's disease, liver degeneration or  
CC osteoarthritis. Note: The present sequence is given in the sequence  
CC listing but is not featured anywhere else in the specification  
XX  
XX Sequence 454 AA;  
SQ

Query Match 99.7%; Score 1558; DB 4; Length 454;  
Best Local Similarity 99.7%; Pred. No. 3.6e-155;  
Matches 295; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KTMNDFYLLKLGKGTGKVLVREKASGKYAMKILKKEVIIAKDEVAHTLTESRVLKN 60  
Db 143 KTMNDFYLLKLGKGTGKVLVREKASGKYAMKILKKEVIIAKDEVAHTLTESRVLKN 202

Qy 61 TRHPFLTSLKYSFQTKORLCFVMEYVNGGELFFHLSRVPFSEDRTFYGAEIVSALDYL 120  
Db 203 TRHPFLTSLKYSFQTKORLCFVMEYVNGGELFFHLSRVPFSEDRTFYGAEIVSALDYL 262

Qy 121 HSGKIVYRDLKLENLMDKOGHIKITDGLCKEGITDAATMKTCGTPGYLAPEVLEDND 180  
Db 263 HSGKIVYRDLKLENLMDKOGHIKITDGLCKEGITDAATMKTCGTPGYLAPEVLEDND 322

Qy 181 YGRAVDWVWGLGVVYEMMCGRLPFYNQDHEKLFELILMEDIKFPRTLSSDAKSLLSGLLI 240  
Db 323 YGRAVDWVWGLGVVYEMMCGRLPFYNQDHEKLFELILMEDIKFPRTLSSDAKSLLSGLLI 382

Qy 241 KDPNKRLLGGGPDPAKEIMRHSFFSGVNWQDVYDKLVPPPKPQVTSFETDTRYFDEE 296  
Db 383 KDPNKRLLGGGPDPAKEIMRHSFFSGVNWQDVYDKLVPPPKPQVTSFETDTRYFDEE 438

GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: February 13, 2006, 06:28:39 ; Search time 426 Seconds  
(without alignments)  
490.226 Million cell updates/sec

Title: US-10-601-311-1\_COPY\_143\_438

Perfect score: 1563

Sequence: 1 KTMNDFYLLKLGKTFKVV.....VPPFKPQVTSIDTRYPDEE 296

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt\_05.80.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query No.	Score	Match %	Length	DB	ID	Description
1	1563	100.0	465	2	Q5VTI2	HUMAN	Q5vti2 homo sapien
2	1563	100.0	466	2	Q56A86	HUMAN	Q56a86 homo sapien
3	1563	100.0	479	1	AKT3	HUMAN	Q9Y243 homo sapien
4	1563	100.0	479	1	AKT3	MOUSE	Q9wua6 mus musculus
5	1563	100.0	479	2	Q5VTI1	HUMAN	Q5vti1 homo sapien
6	1563	100.0	479	2	Q6NWX0	MOUSE	Q6nwx0 mus musculus
7	1568	99.7	454	1	AKT3	RAT	Q63484 rattus norv
8	1428	91.4	523	2	Q4T057	TETNG	Q4t057 tetraodon n
9	1420.5	90.9	480	2	Q57513	CHICK	Q57513 gallus gall
10	1416.5	90.6	481	2	Q98TY9	XENLA	Q98ty9 xenopus lae
11	1402.5	89.7	480	2	Q5ER96	BOVIN	Q5er96 bos taurus
12	1396.5	89.3	1893	2	Q4RLN6	TETNG	Q4rln6 tetraodon n
13	1394.5	89.2	480	1	AKT1	RAT	P47196 rattus norv
14	1394.5	89.2	480	2	Q6GSA6	MOUSE	Q6gsa6 mus musculus
15	1394.5	89.2	501	1	AKT MLVAT		P31748 akt8 murine
16	1394	89.2	479	2	Q8UUX0	BRARE	Q8uux0 brachydanio
17	1393.5	89.2	480	1	AKT1	HUMAN	P31749 homo sapien
18	1391.5	89.0	452	2	Q8BS26	MOUSE	Q8bs26 mus musculus
19	1391.5	89.0	480	1	AKT1	MOUSE	P31750 mus musculus
20	1391	89.0	353	2	Q8CE74	MOUSE	Q8ce74 mus musculus
21	1391	89.0	481	1	AKT2	HUMAN	P31751 homo sapien
22	1391	89.0	481	1	AKT2	MOUSE	Q60823 mus musculus
23	1389	88.9	486	2	Q72X15	XENLA	Q72x15 xenopus lae
24	1386	88.7	485	2	Q61P76	XENLA	Q61p76 xenopus lae
25	1383	88.5	419	2	Q519W5	CANFA	Q519w5 canis faml
26	1380	88.3	472	2	Q4SLA7	TETNG	Q4slat7 tetraodon n
27	1378.5	88.2	480	1	AKT1	BOVIN	Q802Y3 brachydanio
28	1378	88.2	478	2	Q802Y3	BRARE	Q802y3 brachydanio
29	1378	88.2	481	1	AKT2	RAT	P47197 rattus norv
30	1352	80.1	527	2	Q7QK56	ANOAGA	Q7qk56 anopheles g
31	1249	79.9	486	2	Q95YJ0	ASTERINA	Q95yj0 asterina pe

RESULT 1

ID	Q5VTI2_HUMAN	PRELIMINARY;	PRT;	465 AA.
AC	Q5VTI2;			
DT	01-FEB-2005 (Tremblrel. 29, Created)			
DT	01-FEB-2005 (Tremblrel. 29, Last sequence update)			
DT	13-SEP-2005 (Tremblrel. 31, Last annotation update)			
DE	V-akt murine thymoma viral oncogene homolog 3 (protein kinase B, gamma).			
DE	gamma.			
GN	ORFNames=RP11-150L22.2-002;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;			
OC	Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	NUCLEOTIDE SEQUENCE.			
RA	Lad H.;			
RL	Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.			
RN	[2]			
RP	NUCLEOTIDE SEQUENCE.			
RA	Wallis J.;			
RL	Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.			
RN	[3]			
RP	NUCLEOTIDE SEQUENCE.			
RA	Howden P.;			
RL	Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.			
CC	- - CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.			
CC	- - SIMILARITY: Belongs to the Ser/Thr protein kinase family.			
CC	- - SIMILARITY: Contains 1 PH domain.			
DR	EMBL; AL592151; CAH72891.1; -; Genomic DNA.			
DR	EMBL; AL662889; CAH73072.1; -; Genomic DNA.			
DR	EMBL; AL591721; CAH71866.1; -; Genomic DNA.			
DR	EMBL; AC096539; CAH72891.1; JOINED; Genomic DNA.			
DR	EMBL; AL662889; CAH72891.1; JOINED; Genomic DNA.			
DR	EMBL; AL591721; CAH72891.1; JOINED; Genomic DNA.			
DR	EMBL; AL592151; CAH73072.1; JOINED; Genomic DNA.			
DR	EMBL; AL662889; CAH71866.1; JOINED; Genomic DNA.			
DR	EMBL; AL662889; CAH71866.1; JOINED; Genomic DNA.			
DR	EMBL; AC096539; CAH71866.1; JOINED; Genomic DNA.			
DR	EMBL; AL592151; CAH73072.1; JOINED; Genomic DNA.			
DR	EMBL; AC096539; CAH73072.1; JOINED; Genomic DNA.			
DR	SMR; Q5VTI2; 1-115, 144-445.			
DR	Ensembl; ENSG00000117020; Homo sapiens.			
DR	GO; GO:0005524; F:ATP binding; IEA.			
DR	GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.			
DR	GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.			
DR	GO; GO:0006468; P:protein amino acid phosphorylation; IEA.			
DR	InterPro; IPR001849; PH.			
DR	InterPro; IPR011933; PH type.			
DR	InterPro; IPR000961; Pkinase C.			
DR	InterPro; IPR000719; Prot_kinase.			
DR	InterPro; IPR008271; Ser_thr_pkinase.			
DR	InterPro; IPR002290; Ser_thr_pkinase.			

32	1248	79.8	528	2	Q868D7	AEADAE	Q868d7 aedes aegyp
33	1240	79.3	530	2	Q24293	DROME	Q24293 drosophila
34	1240	79.3	530	2	Q24469	DROME	Q24469 drosophila
35	1240	79.3	611	2	Q7JN11	DROME	Q7jnl1 drosophila
36	1240	79.3	611	2	O8INB9	DROME	O8inb9 drosophila
37	1233	78.9	591	2	O4T3K9	TETNG	O4t3k9 tetraodon n
38	1169	74.8	390	2	Q519W4	CANFA	Q519w4 canis faml
39	1118.5	71.6	546	2	Q17942	CAEEL	Q17942 caenorhabdi
40	1104	70.6	532	2	Q61K11	CAEEL	Q61k11 caenorhabdi
41	1098	70.2	541	2	Q17941	CAEEL	Q17941 caenorhabdi
42	1032	66.0	528	2	O9XTG7	CAEEL	O9xtg7 caenorhabdi
43	1027	65.7	483	2	O77145	CAEEL	O77145 caenorhabdi
44	983	62.9	387	2	Q8MUAS	HYDAT	Q8muas hydra atten
45	977	62.5	302	2	Q4TBD9	TETNG	Q4tbd9 tetraodon n

ALIGNMENTS

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DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00169; PH; 1.
DR Pfam; PF00069; Pkinase; 1.
DR Pfam; PF00433; Pkinase_C; 1.
DR SMART; SM00233; PH; 1.
DR SMART; SM00133; S_TK_X; 1.
DR SMART; SM00220; S_TK; 1.
DR SMART; SM00219; TyrKc; 1.
DR PROSITE; PS00003; PH_DOMAIN; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR ATP-binding; Kinase; Nucleotide-binding;
KW Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 465 AA; 54032 MW; 592EF8B6937D1E0 CRC64;

Query Match 100.0%; Score 1563; DB 2; Length 465;
Best Local Similarity 100.0%; Pred. No. 8.6e-96;
Matches 296; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KTMNDFYLLKLGKTFGKVLVREKASGKYAMKILKKEVIIAKDEVAHTLTESRVLKN 60
Db 143 KTMNDFYLLKLGKTFGKVLVREKASGKYAMKILKKEVIIAKDEVAHTLTESRVLKN 202

Qy 61 TRHPFLTSLKYSFQTKDRLCFVMEYVNGGELFFHLSRERFSEDRTRFYGAIEVSALDYL 120
Db 203 TRHPFLTSLKYSFQTKDRLCFVMEYVNGGELFFHLSRERFSEDRTRFYGAIEVSALDYL 262

Qy 121 HSGKIVYRDLKLENLMDKDGHIKITDPLGCKEGITDAATMKTCGTPPEYLAPEVLEND 180
Db 263 HSGKIVYRDLKLENLMDKDGHIKITDPLGCKEGITDAATMKTCGTPPEYLAPEVLEND 322

Qy 181 YGRAVDWGLGVVYEMMCCGRLPFYNQDHEKLFELILMEDIKFPRTLSSDAKSLLSGLLI 240
Db 323 YGRAVDWGLGVVYEMMCCGRLPFYNQDHEKLFELILMEDIKFPRTLSSDAKSLLSGLLI 382

Qy 241 KDPNKRLLGGGPDDAKEIMRHSFFSGVNWQDVYDKLVPPFPKQVTSSTDTRYFDEE 296
Db 383 KDPNKRLLGGGPDDAKEIMRHSFFSGVNWQDVYDKLVPPFPKQVTSSTDTRYFDEE 438

RESULT 2
ID Q56A86 HUMAN PRELIMINARY; PRT; 466 AA.
AC Q56A86;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE AKT3 protein (Fragment).
GN Name=AKT3;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
[1]
RP NUCLEOTIDE SEQUENCE.
RC
RX MEDLINE=22398257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettunen M., Madan A., Rodrigues S., Sanchez A.,
RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
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RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skaleka U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16999-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC
RG NIH MGC Project;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
CC -1- SIMILARITY: Contains 1 PH domain.
DR EMBL; BC020479; AA020479.1; -; mRNA.
DR SMR; Q56A86; 1-115.
DR Ensembl; ENSG00000117020; Homo sapiens.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR001849; PH.
DR InterPro; IPR011993; PH type.
DR InterPro; IPR000961; Pkinase_C.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00169; PH; 1.
DR Pfam; PF00069; Pkinase; 1.
DR Pfam; PF00433; Pkinase_C; 1.
DR SMART; SM00233; PH; 1.
DR SMART; SM00133; S_TK_X; 1.
DR SMART; SM00220; S_TK; 1.
DR SMART; SM00219; TyrKc; 1.
DR PROSITE; PS00003; PH_DOMAIN; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR ATP-binding; Kinase; Nucleotide-binding;
KW Serine/threonine-protein kinase; Transferase.
FT NON TER 466 466
SQ SEQUENCE 466 AA; 54288 MW; CE8576C2B48FCA6E CRC64;

Query Match 100.0%; Score 1563; DB 2; Length 466;
Best Local Similarity 100.0%; Pred. No. 8.6e-96;
Matches 296; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KTMNDFYLLKLGKTFGKVLVREKASGKYAMKILKKEVIIAKDEVAHTLTESRVLKN 60
Db 143 KTMNDFYLLKLGKTFGKVLVREKASGKYAMKILKKEVIIAKDEVAHTLTESRVLKN 202

Qy 61 TRHPFLTSLKYSFQTKDRLCFVMEYVNGGELFFHLSRERFSEDRTRFYGAIEVSALDYL 120
Db 203 TRHPFLTSLKYSFQTKDRLCFVMEYVNGGELFFHLSRERFSEDRTRFYGAIEVSALDYL 262

Qy 121 HSGKIVYRDLKLENLMDKDGHIKITDPLGCKEGITDAATMKTCGTPPEYLAPEVLEND 180
Db 263 HSGKIVYRDLKLENLMDKDGHIKITDPLGCKEGITDAATMKTCGTPPEYLAPEVLEND 322

Qy 181 YGRAVDWGLGVVYEMMCCGRLPFYNQDHEKLFELILMEDIKFPRTLSSDAKSLLSGLLI 240
Db 323 YGRAVDWGLGVVYEMMCCGRLPFYNQDHEKLFELILMEDIKFPRTLSSDAKSLLSGLLI 382

Qy 241 KDPNKRLLGGGPDDAKEIMRHSFFSGVNWQDVYDKLVPPFPKQVTSSTDTRYFDEE 296
Db 383 KDPNKRLLGGGPDDAKEIMRHSFFSGVNWQDVYDKLVPPFPKQVTSSTDTRYFDEE 438

RESULT 3
AKT3_HUMAN
ID AKT3_HUMAN STANDARD; PRT; 479 AA.
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AC Q9Y243; Q96QV3; Q9UPP5;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 13-SEP-2005 (Rel. 48, Last annotation update)  
 DE RAC-gamma serine/threonine-protein kinase (EC 2.7.1.37) (RAC-PK-gamma)  
 DE (Protein kinase Akt-3) (Protein kinase B, gamma) (PKB gamma) (SFK-2).  
 GN Name=AKT3;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
 OC Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RN NUCLEOTIDE SEQUENCE, AND MUTAGENESIS.  
 RP MEDLINE=99194749; PubMed=10092583; DOI=10.1074/jbc.274.14.9133;  
 RA Brodbeck D., Cron P., Hemmings B.A.;  
 RT "A human protein kinase B gamma with regulatory phosphorylation sites  
 in the activation loop and in the C-terminal hydrophobic domain.";  
 RL J. Biol. Chem. 274:9133-9136(1999).  
 RN [2]  
 RN NUCLEOTIDE SEQUENCE.  
 RP MEDLINE=99252329; PubMed=10208883; DOI=10.1006/bbrc.1999.0559;  
 RA Nakatani K., Sakaue H., Thompson D.A., Weigel R.J., Roth R.A.;  
 RT "Identification of a human Akt3 (protein kinase B gamma) which  
 contains the regulatory serine phosphorylation site.";  
 RL Biochem. Biophys. Res. Commun. 257:906-910(1999).  
 RN [3]  
 RN TISSUE=Brain;  
 RP MEDLINE=99421751; PubMed=10491192;  
 RA Masure S., Haefner B., Wesseling J.-J., Hoefnagel E., Mortier E.,  
 RA Verhassel P., Tuytelaars A., Gordon R., Richardson A.;  
 RT "Molecular cloning, expression and characterization of the human  
 serine/threonine kinase Akt-3.";  
 RL Eur. J. Biochem. 265:353-360(1999).  
 RN [4]  
 RN NUCLEOTIDE SEQUENCE (ISOFORM 1).  
 RP Li X., Yu L., Huang H., Zhang M., Zhao Y., Zhao S.;  
 RT "Cloning of a novel human cDNA, STK-2, which encodes a rat serine-  
 threonine protein kinase (STK) homolog.";  
 RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.  
 RN [5]  
 RN NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM 2).  
 RP TISSUE=Testis;  
 RA MEDLINE=21154917; PubMed=11230166; DOI=10.1101/gr.154701;  
 RA Wiemann S., Weil B., Wellenreuther R., Gassenhuber J., Glassl S.,  
 RA Ansong M., Boecker M., Bloeker H., Bauersachs S., Blum H.,  
 RA Lauber J., Duesterhoeft A., Beyer A., Koehrer K., Strack N.,  
 RA Mewes H.-W., Ottenwaelder B., Obermaier B., Tampe J., Heubner D.,  
 RA Wambutt R., Korn B., Klein M., Poustka A.;  
 RT "Towards a catalog of human genes and proteins: sequencing and  
 analysis of 500 novel complete protein coding human cDNAs.";  
 RL Genome Res. 11:422-435(2001).  
 RN [6]  
 RN NUCLEOTIDE SEQUENCE (ISOFORMS 1 AND 2), AND MUTAGENESIS OF THR-305 AND  
 THR-447.  
 RP PubMed=11387345; DOI=10.1074/jbc.M104633200;  
 RA Brodbeck D., Hill M.M., Hemmings B.A.;  
 RT "Two splice variants of PKB gamma have different regulatory capacity  
 depending on the presence or absence of the regulatory phosphorylation  
 site Ser-472 in the C-terminal hydrophobic domain.";  
 RL J. Biol. Chem. 276:29550-29558(2001).  
 CC -!- FUNCTION: IGF-1 leads to the activation of AKT3, which may play a  
 role in regulating cell survival. Capable of phosphorylating  
 several known proteins. Truncated isoform 2/PKB gamma 1 without  
 the second serine phosphorylation site could still be stimulated  
 but to a lesser extent.  
 CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.  
 CC -!- INTERACTION:  
 CC Q16543: CDC37; NbExp=1; IntAct=EBI-296115; EBI-295634;  
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic and membrane-associated after  
 cell stimulation leading to its translocation.  
 CC -!- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=2;  
 CC Name=1; Synonyms=PKB gamma;  
 CC IsoId=Q9Y243-1; Sequence=Displayed;  
 CC Name=2; Synonyms=PKB gamma 1;  
 CC IsoId=Q9Y243-2; Sequence=VSP\_004947;  
 CC -!- TISSUE SPECIFICITY: In adult tissues, it is highly expressed in  
 brain, lung and kidney, but weakly in heart, testis and liver. In  
 fetal tissues, it is highly expressed in heart, liver and brain  
 and not at all in kidney.  
 CC -!- DOMAIN: Binding of the PH domain to the phosphatidylinositol 3-  
 kinase alpha (PI(3)K) results in its targeting to the plasma  
 membrane.  
 CC -!- PTM: Phosphorylated on threonine and serine residues.  
 CC Phosphorylation on both serines and threonines is required for  
 full activity.  
 CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family. RAC  
 subfamily.  
 CC -!- SIMILARITY: Contains 1 PH domain.  
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
 between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 the European Bioinformatics Institute. There are no restrictions on its  
 use as long as its content is in no way modified and this statement is not  
 removed.  
 DR EMBL; AF124141; AAD29089.1; -; mRNA.  
 DR EMBL; AF135794; AAD24196.1; -; mRNA.  
 DR EMBL; AF085234; AAL40392.1; -; mRNA.  
 DR EMBL; AJ245709; CAB53537.1; -; mRNA.  
 DR EMBL; AL117525; CAB55977.1; ALT TERM; mRNA.  
 DR EMBL; AY005799; AAF91073.1; -; mRNA.  
 DR PIR; A59380; A59380.  
 DR HSSP; P31751; IGZK.  
 DR SMR; Q9Y243; 1-115.  
 DR IntAct; Q9Y243; -.  
 DR Ensembl; ENSG00000117020; Homo sapiens.  
 DR HGNC; HGNC:393; AKT3.  
 DR GO; GO:0004672; P:protein kinase activity; TAS.  
 DR GO; GO:0006468; P:protein amino acid phosphorylation; TAS.  
 DR GO; GO:0007165; P:signal transduction; TAS.  
 DR InterPro; IPR001849; PH.  
 DR InterPro; IPR011993; PH type.  
 DR InterPro; IPR000961; Pkinase\_C.  
 DR InterPro; IPR000719; Prot\_kinase.  
 DR InterPro; IPR008271; Ser\_thr\_pkin\_AS.  
 DR InterPro; IPR002290; Ser\_thr\_pkinase.  
 DR Pfam; PF00169; PH; 1.  
 DR Pfam; PF00069; Pkinase; 1.  
 DR Pfam; PF00433; Pkinase\_C; 1.  
 DR ProDom; PD000001; Prot\_kinase; 1.  
 DR SMART; SM00233; PH; 1.  
 DR SMART; SM00133; S\_TK\_X; 1.  
 DR SMART; SM00220; S\_TKG; 1.  
 DR PROSITE; PS50003; PH\_DOMAIN; 1.  
 DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
 KW Alternative splicing; ATP-binding; Kinase; Nucleotide-binding;  
 KW Phosphorylation; Serine/threonine-protein kinase; Transferase.  
 FT DOMAIN 5 107  
 FT NP\_BIND 148 405 Protein kinase.  
 FT ACT\_SITE 271 271 ATP (By similarity).  
 FT BINDING 177 177 Proton acceptor (By similarity).  
 FT MOD\_RES 305 305 ATP (By similarity).  
 FT MOD\_RES 472 472 Phosphothreonine (By similarity).  
 FT MOD\_RES 472 472 Phosphoserine (By similarity).  
 FT VARSPPLIC 452 479 YDEGMDCMNERRRHHFPQFSASGRE -> CQSQDCGML  
 GNWKK (in isoform 2).  
 FT FTID=VSP\_004947.  
 FT T->A: No activation after pervanadate  
 treatment.  
 FT T->D: 2-fold increase of phosphorylation  
 steady state level, no activation after  
 treatment.

```
FT MUTAGEN 447 447 pervanadate treatment.
FT T->A: No effect.
FT MUTAGEN 447 447 T->D: No effect.
FT MUTAGEN 472 472 S->A: 67% decrease of activity after
FT pervanadate treatment.
FT MUTAGEN 472 472 S->D: 1.4-fold increase of
FT phosphorylation steady state level, 50%
FT decrease of activity after pervanadate
FT treatment.
SQ SEQUENCE 479 AA; 55775 MW; F08BDD6502E78FB CRC64;

Query Match 100.0%; Score 1563; DB 1; Length 479;
Best Local Similarity 100.0%; Pred. No. 8.9e-96;
Matches 296; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KTWNDFYLLKLGKGTGFKVILVREKASGKYAMKILKKEVIIAKDEVAHTLTESRVLKN 60
Db 143 KTWNDFYLLKLGKGTGFKVILVREKASGKYAMKILKKEVIIAKDEVAHTLTESRVLKN 202

Qy 61 TRHPFLTSLKYSFQTKDRLCFVMEYVNGGELFFHLSSRVFSEDRTRFYGAIEVSALDYL 120
Db 203 TRHPFLTSLKYSFQTKDRLCFVMEYVNGGELFFHLSSRVFSEDRTRFYGAIEVSALDYL 262

Qy 121 HSGKIVYRDLKLENMLDKDGHKIKITDFGLCKEGITDAATMKTCGTPPEYLAPVLEND 180
Db 263 HSGKIVYRDLKLENMLDKDGHKIKITDFGLCKEGITDAATMKTCGTPPEYLAPVLEND 322

Qy 181 YGRAVDWVWGLGVVMEYVNGGRLPFYNQDHEKLFELIMEDIKFPRTLSSDAKSLLSGLLI 240
Db 323 YGRAVDWVWGLGVVMEYVNGGRLPFYNQDHEKLFELIMEDIKFPRTLSSDAKSLLSGLLI 382

Qy 241 KDPNKRLLGGGDDAKEIMRHSEFFSGVNMQDVYDKLVPPFPQVTSSETDTRFYDDE 296
Db 383 KDPNKRLLGGGDDAKEIMRHSEFFSGVNMQDVYDKLVPPFPQVTSSETDTRFYDDE 438

RESULT 4
ID AKT3 MOUSE STANDARD; PRT; 479 AA.
AC Q9WUA6:
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE RAC-gamma serine/threonine-protein kinase (EC 2.7.1.37) (RAC-PK-gamma)
DE (Protein Kinase Akt-3) (Protein kinase B, gamma) (pKB gamma).
GN Name=Akt3;
OS Mus musculus (Mouse);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]_
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=99194749; PubMed=10092583; DOI=10.1074/jbc.274.14.9133;
RA Brodbeck D., Cron P., Hemmings B.A.;
RT "A human protein kinase B gamma with regulatory phosphorylation sites
RT in the activation loop and in the C-terminal hydrophobic domain.";
RL J. Biol. Chem. 274:9133-9136(1999).
RN [2]_
RP NUCLEOTIDE SEQUENCE (ISOFORMS 1 AND 2).
RC TISSUE=Brain;
RX PubMed=11387345; DOI=10.1074/jbc.M104633200;
RA Brodbeck D., Hill M.M., Hemmings B.A.;
RT "Two splice variants of PKB gamma have different regulatory capacity
RT depending on the presence or absence of the regulatory phosphorylation
RT site Ser-472 in the C-terminal hydrophobic domain.";
RL J. Biol. Chem. 276:29550-29558(2001).
CC -|- FUNCTION: IGF-1 leads to the activation of AKT3, which may play a
CC role in regulating cell survival. Capable of phosphorylating
CC several known proteins. Truncated isoform 2/pKB gamma 1 without
CC the second serine phosphorylation site could still be stimulated
CC but to a lesser extent (By similarity).
CC -|- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
```

```
CC -|- SUBCELLULAR LOCATION: Cytoplasmic and membrane-associated after
CC cell stimulation leading to its translocation.
CC -|- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1; Synonyms=PKB gamma;
CC IsoId=Q9WUA6-1; Sequence=Displayed;
CC Name=2; Synonyms=PKB gamma 1;
CC IsoId=Q9WUA6-2; Sequence=VSP_004948;
CC -|- TISSUE SPECIFICITY: Isoform 1 is expressed in prostate, testis,
CC uterus and mammary gland and isoform 2 is expressed in prostate,
CC testis and mammary gland.
CC -|- DOMAIN: Binding of the PH domain to the phosphatidylinositol 3-
CC kinase alpha (PI(3)K) results in its targeting to the plasma
CC membrane.
CC -|- PTM: Phosphorylated on threonine and serine residues.
CC Phosphorylation on both sites is required for full activity.
CC -|- SIMILARITY: Belongs to the Ser/Thr protein kinase family. RAC
CC subfamily.
CC -|- SIMILARITY: Contains 1 PH domain.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; AF124142; AAD29090.1; -; mRNA.
CC HSP; P31751; IGZK.
CC SMR; Q9WUA6; 1-115.
CC Ensembl; ENSMUSG00000019699; Mus musculus.
CC MGI; MGI:1345147; Akt3.
CC InterPro; IPR001849; PH.
CC InterPro; IPR011993; PH type.
CC InterPro; IPR000961; Kinase_C.
CC InterPro; IPR000719; Prot_kinase.
CC InterPro; IPR008271; Ser_thr_pkin_AS.
CC Pfam; PF00169; PH; 1.
CC Pfam; PF00069; Kinase; 1.
CC Pfam; PF00433; Kinase_C; 1.
CC ProDom; PD000001; Prot_kinase; 1.
CC PROSITE; PS00003; PH DOMAIN; 1.
CC PROSITE; PS00107; PROTEIN KINASE ATP; 1.
CC PROSITE; PS00011; PROTEIN KINASE DOM; 1.
CC PROSITE; PS00108; PROTEIN KINASE ST; 1.
CC KW Alternative splicing; ATP-binding; Kinase; Nucleotide-binding;
CC Phosphorylation; Serine/threonine-protein kinase; Transferase.
FT DOMAIN 5 107 PH.
FT DOMAIN 148 405 Protein kinase.
FT NP_BIND 154 162 ATP (By similarity).
FT ACT_SITE 271 271 Proton acceptor (By similarity).
FT BINDING 177 177 ATP (By similarity).
FT MOD_RES 305 305 Phosphothreonine (By similarity).
FT MOD_RES 472 472 Phosphoserine (By similarity).
FT VARSP 452 479 YDDGDMGDMNRPRPFPQFSYASGRE -> CQQSDCGML
FT /FTID=VSP_004948.
FT /FTID=VSP_004948.
SQ SEQUENCE 479 AA; 55714 MW; F08ACDF75743B8FB CRC64;

Query Match 100.0%; Score 1563; DB 1; Length 479;
Best Local Similarity 100.0%; Pred. No. 8.9e-96;
Matches 296; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KTWNDFYLLKLGKGTGFKVILVREKASGKYAMKILKKEVIIAKDEVAHTLTESRVLKN 60
Db 143 KTWNDFYLLKLGKGTGFKVILVREKASGKYAMKILKKEVIIAKDEVAHTLTESRVLKN 202

Qy 61 TRHPFLTSLKYSFQTKDRLCFVMEYVNGGELFFHLSSRVFSEDRTRFYGAIEVSALDYL 120
Db 203 TRHPFLTSLKYSFQTKDRLCFVMEYVNGGELFFHLSSRVFSEDRTRFYGAIEVSALDYL 262

Qy 121 HSGKIVYRDLKLENMLDKDGHKIKITDFGLCKEGITDAATMKTCGTPPEYLAPVLEND 180
Db 263 HSGKIVYRDLKLENMLDKDGHKIKITDFGLCKEGITDAATMKTCGTPPEYLAPVLEND 322
```

QY 181 YGRAVDWGLGVVYEMMCGRLPFYNQDHEKLFELILMEDIKFPRTLSSDAKSLLSGLLI 240  
 |||||  
 DB 323 YGRAVDWGLGVVYEMMCGRLPFYNQDHEKLFELILMEDIKFPRTLSSDAKSLLSGLLI 382  
 |||||  
 QY 241 KDPNKRLLGGPDDAKEIMRHSFFSGVNMQDVYDKLVPPFPQVTSSETDTRYFDEE 296  
 |||||  
 DB 383 KDPNKRLLGGPDDAKEIMRHSFFSGVNMQDVYDKLVPPFPQVTSSETDTRYFDEE 438  
 |||||

RESULT 5  
 Q5VT11 HUMAN  
 ID Q5VT11\_HUMAN PRELIMINARY; PRT; 479 AA.  
 AC Q5VT11  
 DT 01-FEB-2005 (TRENBLrel. 29, Created)  
 DT 01-FEB-2005 (TRENBLrel. 29, Last sequence update)  
 DT 13-SEP-2005 (TRENBLrel. 31, Last annotation update)  
 DE V-akt murine thymoma viral oncogene homolog 3 (Protein kinase B, gamma)  
 GN ORFNames=RP11-150122.2-001;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
 OC Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Lad H.;  
 RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Wallis J.;  
 RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Howden P.;  
 RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.  
 CC -|- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.  
 CC -|- SIMILARITY: Belongs to the Ser/Thr protein kinase family.  
 CC -|- SIMILARITY: Contains 1 PH domain.  
 DR EMBL; AL592151; CAH72892.1; -; Genomic DNA.  
 DR EMBL; AL662889; CAH73073.1; -; Genomic DNA.  
 DR EMBL; AL591721; CAH71867.1; -; Genomic DNA.  
 DR EMBL; AC096539; CAH72892.1; JOINED; Genomic DNA.  
 DR EMBL; AL662889; CAH72892.1; JOINED; Genomic DNA.  
 DR EMBL; AL591721; CAH72892.1; JOINED; Genomic DNA.  
 DR EMBL; AL591721; CAH73073.1; JOINED; Genomic DNA.  
 DR EMBL; AL592151; CAH71867.1; JOINED; Genomic DNA.  
 DR EMBL; AL662889; CAH71867.1; JOINED; Genomic DNA.  
 DR EMBL; AC096539; CAH71867.1; JOINED; Genomic DNA.  
 DR EMBL; AL592151; CAH73073.1; JOINED; Genomic DNA.  
 DR EMBL; AC096539; CAH73073.1; JOINED; Genomic DNA.  
 DR SMR; Q5VT11; 1-115.  
 DR Ensemble; ENSG00000117020; Homo sapiens.  
 DR GO; GO:0005524; F:ATP binding; IEA.  
 DR GO; GO:004674; F:Protein serine/threonine kinase activity; IEA.  
 DR GO; GO:0004713; F:Protein-tyrosine kinase activity; IEA.  
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.  
 DR InterPro; IPR001849; PH.  
 DR InterPro; IPR001993; PH type.  
 DR InterPro; IPR000961; Kinase C.  
 DR InterPro; IPR000719; Prot kinase.  
 DR InterPro; IPR008271; Ser thr pkin AS.  
 DR InterPro; IPR002290; Ser thr pkinase.  
 DR InterPro; IPR001245; Tyr\_pkinase.  
 DR Pfam; PF00169; PH; 1.  
 DR Pfam; PF00069; Kinase; 1.  
 DR Pfam; PF00433; Kinase C; 1.  
 DR SMART; SM00233; PH; 1.  
 DR SMART; SM00133; S\_TK\_X; 1.  
 DR SMART; SM00220; S\_TKC; 1.  
 DR SMART; SM00219; TYRK; 1.  
 DR PROSITE; PS50003; PH\_DOMAIN; 1.

DR PROSITE; PS00107; PROTEIN KINASE\_ATP; 1.  
 DR PROSITE; PS50011; PROTEIN KINASE\_DOM; 1.  
 DR PROSITE; PS00108; PROTEIN KINASE\_ST; 1.  
 KW ATP-binding; Kinase; Nucleotide-binding;  
 KW Serine/threonine-protein kinase; Transferase.  
 SQ SEQUENCE 479 AA; 55775 MW; F08BDD6502E78PB CRC64;  
 |||||

Query Match 100.0%; Score 1563; DB 2; Length 479;  
 Best Local Similarity 100.0%; Pred. No. 8.9e-96;  
 Matches 296; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KTMNDFYLLKLLGKGTGKVLVREKASGKYAMKILKKEVIAKDEVAHTLTESRLKN 60  
 |||||  
 DB 143 KTMNDFYLLKLLGKGTGKVLVREKASGKYAMKILKKEVIAKDEVAHTLTESRLKN 202  
 |||||

QY 61 TRHPFLTSKYSFQKRLCFVMEYVNGGELFFHLSSRRVSESDTRFYGAIEIVSALDYL 120  
 |||||  
 DB 203 TRHPFLTSKYSFQKRLCFVMEYVNGGELFFHLSSRRVSESDTRFYGAIEIVSALDYL 262  
 |||||

QY 121 HSGKIVYRDIALENMLDKDGHIKITDFGLCKEGITDAATMKTFCGTPEYLAPVLEND 180  
 |||||  
 DB 263 HSGKIVYRDIALENMLDKDGHIKITDFGLCKEGITDAATMKTFCGTPEYLAPVLEND 322  
 |||||

QY 181 YGRAVDWGLGVVYEMMCGRLPFYNQDHEKLFELILMEDIKFPRTLSSDAKSLLSGLLI 240  
 |||||  
 DB 323 YGRAVDWGLGVVYEMMCGRLPFYNQDHEKLFELILMEDIKFPRTLSSDAKSLLSGLLI 382  
 |||||

QY 241 KDPNKRLLGGPDDAKEIMRHSFFSGVNMQDVYDKLVPPFPQVTSSETDTRYFDEE 296  
 |||||  
 DB 383 KDPNKRLLGGPDDAKEIMRHSFFSGVNMQDVYDKLVPPFPQVTSSETDTRYFDEE 438  
 |||||

RESULT 6  
 Q6NXW0 MOUSE  
 ID Q6NXW0\_MOUSE PRELIMINARY; PRT; 479 AA.  
 AC Q6NXW0  
 DT 05-JUL-2004 (TRENBLrel. 27, Created)  
 DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)  
 DE Thymoma viral proto-oncogene 3.  
 GN Name=Akt3;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridea; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=CD1; TISSUE=Neural Stem Cell;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A.C., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grumwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences."  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=CD1; TISSUE=Neural Stem Cell;

RA Director MGC Project;  
 RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.  
 CC -|- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.  
 CC -|- SIMILARITY: Belongs to the Ser/Thr protein kinase family.  
 CC -|- SIMILARITY: Contains 1 PH domain.  
 DR EMBL; BC068661; AAH66861.1; -; mRNA.  
 DR HSSP; P05132; 1APM.  
 DR SMR; Q6NWX0; 1-115.  
 DR Ensembl; ENSMUSG00000019699; Mus musculus.  
 DR MGI; MGI:1345147; Akt3.  
 DR GO; GO:0005524; F:ATP binding; IEA.  
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.  
 DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.  
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.  
 DR InterPro; IPR001849; PH.  
 DR InterPro; IPR011993; PH type.  
 DR InterPro; IPR000961; Pkinase\_C.  
 DR InterPro; IPR000719; Prot\_kinase.  
 DR InterPro; IPR008271; Ser\_thr\_pkin\_AS.  
 DR InterPro; IPR002290; Ser\_thr\_pkinase.  
 DR InterPro; IPR001245; Tyr\_pkinase.  
 DR Pfam; PF00169; PH; 1.  
 DR Pfam; PF00069; Pkinase; 1.  
 DR Pfam; PF00433; Pkinase\_C; 1.  
 DR ProDom; PD000001; Prot\_kinase; 1.  
 DR SMART; SM00233; PH; 1.  
 DR SMART; SM00133; S TK X; 1.  
 DR SMART; SM00220; S\_TKC; 1.  
 DR SMART; SM00219; TyrKC; 1.  
 DR PROSITE; PS50003; PH DOMAIN; 1.  
 DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.  
 DR PROSITE; PS00111; PROTEIN KINASE DOM; 1.  
 DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
 KW ATP-binding; Kinase; Nucleotide-binding;  
 KW Serine/threonine-protein kinase; Transferase.  
 SQ SEQUENCE 479 AA; 55657 MW; FA31AC734651B92D CRC64;

Query Match 100.0%; Score 1563; DB 2; Length 479;  
 Best Local Similarity 100.0%; Pred. No. 8,9e-96;  
 Matches 296; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KTNWDFYLLKLGKGTGKVLVREKASGKYAMKILKKEVIAKDEVAHTLTESRLVN 60  
 Db 143 KTNWDFYLLKLGKGTGKVLVREKASGKYAMKILKKEVIAKDEVAHTLTESRLVN 202

Qy 61 TRHPFLTSLKYSFQTKORLCFVMEVYNGGELFFHLSERVSEDRTRFYGABIVSALDYL 120  
 Db 203 TRHPFLTSLKYSFQTKORLCFVMEVYNGGELFFHLSERVSEDRTRFYGABIVSALDYL 262

Qy 121 HSGKIVYRDLKLEMLDKDGHKIKITDFGLCKEGITDAATMKTFCGTPPYLAPVLESDND 180  
 Db 263 HSGKIVYRDLKLEMLDKDGHKIKITDFGLCKEGITDAATMKTFCGTPPYLAPVLESDND 322

Qy 181 YGRAVDWVGLGVVYEMWCGRLPFYNQDHEKLFELLMEDIKFPRTLSDDAKSLLSGLLI 240  
 Db 323 YGRAVDWVGLGVVYEMWCGRLPFYNQDHEKLFELLMEDIKFPRTLSDDAKSLLSGLLI 382

Qy 241 KDPNKRLLGGGDDDAKEINRHSFFSGVNWQDYDKLVPPPKPQVTSSETDTRYPDEE 296  
 Db 383 KDPNKRLLGGGDDDAKEINRHSFFSGVNWQDYDKLVPPPKPQVTSSETDTRYPDEE 438

RESULT 7  
 AKT3\_RAT  
 ID AKT3\_RAT  
 AC Q63484;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 13-SEP-2005 (Rel. 48, Last sequence update)  
 DT 13-SEP-2005 (Rel. 48, Last annotation update)  
 DE RAC-gamma serine/threonine-protein kinase (EC 2.7.1.37) (RAC-PK-gamma)  
 DE (Protein kinase Akt-3) (Protein kinase B, gamma) (PKB gamma).  
 GN Name=Akt3;  
 OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridea; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Brain;  
 RX MEDLINE=96063640; PubMed=7488143;  
 RA Konishi H., Kuroda S., Tanaka M., Matsuzaki H., Ono Y., Kameyama K.,  
 HA Haga T., Kikkawa U.,  
 RT "Molecular cloning and characterization of a new member of the RAC  
 RT protein kinase family: association of the pleckstrin homology domain  
 RT of three types of RAC protein kinase with protein kinase C subtypes  
 RT and beta gamma subunits of G proteins.";  
 RL Biochem. Biophys. Res. Commun. 216:526-534(1995).  
 CC -|- FUNCTION: IGF-1 leads to the activation of AKT3, which may play a  
 CC role in regulating cell survival. Capable of phosphorylating  
 CC several known proteins (By similarity).  
 CC -|- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.  
 CC -|- DOMAIN: Binding of the PH domain to the phosphatidylinositol 3-  
 CC kinase alpha (PI(3)K) results in its targeting to the plasma  
 CC membrane.  
 CC -|- PM: Phosphorylated on threonine and serine residues.  
 CC Phosphorylation on both sites is required for full activity.  
 CC -|- SIMILARITY: Belongs to the Ser/Thr protein kinase family. RAC  
 CC subfamily.  
 CC -|- SIMILARITY: Contains 1 PH domain.  
 CC -----  
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 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -  
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 CC use as long as its content is in no way modified and this statement is not  
 CC removed.  
 CC -----  
 DR EMBL; D49836; BAA08637.1; -; mRNA.  
 DR PIR; JC4345; JC4345.  
 DR HSSP; P31751; 1GZK.  
 DR SMR; Q63484; 1-115, 144-445.  
 DR RGD; 62390; Akt3.  
 DR GO; GO:0005515; F:protein binding; IDA.  
 DR GO; GO:0005080; F:protein kinase C binding; IDA.  
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; IDA.  
 DR InterPro; IPR01849; PH.  
 DR InterPro; IPR011993; PH type.  
 DR InterPro; IPR000961; Pkinase\_C.  
 DR InterPro; IPR000719; Prot\_kinase.  
 DR InterPro; IPR008271; Ser\_thr\_pkin\_AS.  
 DR Pfam; PF00169; PH; 1.  
 DR Pfam; PF00069; Pkinase; 1.  
 DR Pfam; PF00433; Pkinase\_C; 1.  
 DR ProDom; PD000001; Prot\_kinase; 1.  
 DR PROSITE; PS50003; PH DOMAIN; 1.  
 DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.  
 DR PROSITE; PS00108; PROTEIN KINASE DOM; 1.  
 DR PROSITE; PS00111; PROTEIN\_KINASE\_ST; 1.  
 KW ATP-binding; Kinase; Nucleotide-binding; Phosphorylation;  
 KW Serine/threonine-protein kinase; Transferase.  
 FT DOMAIN 5 107 PH.  
 FT DOMAIN 148 405 Protein kinase.  
 FT NP\_BIND 154 162 ATP (By similarity).  
 FT ACT\_SITE 271 271 Proton acceptor (By similarity).  
 FT BINDING 177 177 ATP (By similarity).  
 FT MOD\_RES 305 305 Phosphothreonine (By similarity).  
 SQ SEQUENCE 454 AA; 52850 MW; 68072CF9DFEE876 CRC64;

Query Match 99.7%; Score 1558; DB 1; Length 454;  
 Best Local Similarity 99.7%; Pred. No. 1.8e-95;  
 Matches 295; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KTNWDFYLLKLGKGTGKVLVREKASGKYAMKILKKEVIAKDEVAHTLTESRLVN 60  
 Db 143 KTNWDFYLLKLGKGTGKVLVREKASGKYAMKILKKEVIAKDEVAHTLTESRLVN 202



QY 61 TRHPFLTSIKYSFOTKDRLCFVMEYVNGELFFHLRSRVFSEDTREYGAIVSALDYL 120  
 DB 203 TRHPFLTSIKYSFOTKDRLCFVMEYVNGELFFHLRSRVFSEDTREYGAIVSALDYL 262  
 QY 121 HSGKIVYRDLEKLEMLDKDGHKIKITDFGLCKEGITDAATMTKTCGTPYLAPVLEND 180  
 DB 263 HSGKIVYRDLEKLEMLDKDGHKIKITDFGLCKEGITDAATMTKTCGTPYLAPVLEND 322  
 QY 181 YGRAVDWGLGVVYEMMCGRLFFYNQDHEKLFELILMEDIKFPRTLSSDAKSLLSGLLI 240  
 DB 323 YGRAVDWGLGVVYEMMCGRLFFYNQDHEKLFELILMEDIKFPRTLSSDAKSLLSGLLI 382  
 QY 241 KDPNKRLLGGPPDDAKEIMRHSFSGVNMQDVYDKLVPPKPVQVTSDDTRYFDEE 296  
 DB 383 KDPNKRLLGGPPDDAKEIMRHSFSGVNMQDVYDKLVPPKPVQVTSDDTRYFDEE 438

RESULT 8  
 Q4T057\_TETNG  
 ID Q4T057\_TETNG PRELIMINARY; PRT; 523 AA.  
 AC Q4T057;  
 DT 13-SEP-2005 (TReMBLrel. 31, Created)  
 DT 13-SEP-2005 (TReMBLrel. 31, Last sequence update)  
 DT 13-SEP-2005 (TReMBLrel. 31, Last annotation update)  
 DE Chromosome undetermined SCAP11339, whole genome shotgun sequence.  
 DE (Fragment).  
 GN ORFNames=GSTENG0009507001;  
 OS Tetraodon nigroviridis (Green puffer).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
 OC Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;  
 OC Tetraodontidae; Tetraodontidae; Tetraodon.  
 OX NCBI\_TaxID=99883;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,  
 RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,  
 RA Nicaud S., Jaife D., Fisher S., Lutfalla G., Dossat C., Segurens B.,  
 RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,  
 RA Anthouard V., Jubin C., Castellani V., Katinka M., Vacherie B.,  
 RA Biemont C., Skalli Z., Catolico L., Poulain J., De Berardinis V.,  
 RA Cruaud C., Duprat S., Brotier P., Coutanceau J.P., Gouzy J.,  
 RA Parra G., Lardier G., Chapelle C., McKernan K.J., McEwan P., Bosak S.,  
 RA Kellis M., Volff J.N., Guigo R., Zody M.C., Mesirov J.,  
 RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,  
 RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,  
 RA Winkler P., Lander E.S., Weissbach J., Roest Crolius H.,  
 RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals  
 the early vertebrate proto-karyotype."  
 RL Nature 431:946-957(2004).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RG Genoscope; Whitehead Institute Centre for Genome Research;  
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.  
 CC -!- CAUTION: The sequence shown here is derived from an  
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is  
 CC preliminary data.  
 CC -!- FUNCTION: Plays a key role in the control of the eukaryotic cell  
 CC cycle. It is required in higher cells for entry into S-phase and  
 CC mitosis. Component of the kinase complex that phosphorylates the  
 CC repetitive C-terminus of RNA polymerase II. Catalytic component of  
 CC MPF (By similarity).  
 CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.  
 CC -!- SUBUNIT: Forms a stable but non-covalent complex with cyclin B in  
 CC mature oocytes (By similarity).  
 CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.  
 CC -!- SIMILARITY: Contains 1 PH domain.  
 DR EMBL; CAAB01011339; CAF93725.1; -; Genomic\_DNA.  
 DR InterPro; IPR001849; PH.  
 DR InterPro; IPR000961; Pkinase C.  
 DR InterPro; IPR000719; Prot\_kinase.  
 DR InterPro; IPR008271; Ser\_Thr\_pkin\_AS.  
 DR InterPro; IPR002290; Ser\_Thr\_pkinase.

InterPro; IPR001245; Tyr\_pkinase.  
 Pfam; PF00169; PH; 1.  
 Pfam; PF00069; Pkinase; 1.  
 Pfam; PF00433; Pkinase\_C; 1.  
 DR ProDom; PD000001; Prot\_kinase; 1.  
 DR SMART; SM00233; PH; 1.  
 DR SMART; SM00133; S\_TK\_X; 1.  
 DR SMART; SM00220; S\_TK; 1.  
 DR SMART; SM00219; TyrKc; 1.  
 DR PROSITE; PS00003; PH DOMAIN; 1.  
 DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE; PS00111; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
 KW ATP-binding; Kinase; Nucleotide-binding;  
 KW Serine/threonine-protein kinase; Transferase.  
 FT NON TER 523  
 SQ SEQUENCE 523 AA; 60242 MW; D2FC6BED3B92090F CRC64;

Query Match 91.4%; Score 1428; DB 2; Length 523;  
 Best Local Similarity 81.5%; Pred. No. 9.1e-87;  
 Matches 277; Conservative 8; Mismatches 11; Indels 44; Gaps 2;  
 QY 1 KTMNDFDYLLKLGKGTGKVLVREKASGKYAMKILKKEVIIAKDEVAHLLTESRVLKN 60  
 DB 143 KTMNDFDYLLKLGKGTGKVLVREKASGTYAMKILKKEVIIAKDEVAHLLTESRVLKN 202  
 QY 61 TRHPFLT-----SLKYSFOTKDRLCFVMEYVNGE----- 90  
 DB 203 TRHPFLTVSTAWRRRRRGAGSDRCLSVCLQSLKRRKDRLCFVMEYVNGEVRAGGSDVLC 262  
 QY 91 -----LFFHLRSRVFSEDTREYGAIVSALDYLHSGKIVYRDLEKLEML 136  
 DB 263 RGRCVTRVLSPPQLFFHLRSRVFSEDTREYGAIVSALDYLHSGKIVYRDLEKLEML 322  
 QY 137 LDKDGHKIKITDFGLCKEGITDAATMTKTCGTPYLAPVLENDYGRAVDWGLGVVME 196  
 DB 323 LDKDGHKIKITDFGLCKEGITDAATMTKTCGTPYLAPVLENDYGRGVDMWGLGVVME 382  
 QY 197 MMCRLPFYNQDHEKLFELILMEDIKFPRTLSSDAKSLLSGLLIKDPNKRLLGGPPDDAKE 256  
 DB 383 MMCRLPFYNQDHEKLFELILMEBIKFPRTLSSDAKSLLSGLLIKDPNKRLLGGPPDDAKE 442  
 QY 257 IMRHSFSGVNMQDVYDKLVPPKPVQVTSDDTRYFDEE 296  
 DB 443 IMRHSFSTIDMQDLYDKLVPPFPQVTSDDTRYFDEE 482

RESULT 9  
 OS7513\_CHICK  
 ID OS7513\_CHICK PRELIMINARY; PRT; 480 AA.  
 AC OS7513;  
 DT 01-JUN-1998 (TReMBLrel. 06, Created)  
 DT 01-JUN-1998 (TReMBLrel. 06, Last sequence update)  
 DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)  
 DE Serine/threonine protein kinase.  
 GN Name=akti;  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus  
 OX NCBI\_TaxID=9031;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RA Theelen M., Swinkels S.U.M., de Jong M.D.M., Thomas A.A.M.,  
 RA Verkleij A.J., Hanafusa H., Humbel B.,  
 RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.  
 CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.  
 CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.  
 CC -!- SIMILARITY: Contains 1 PH domain.  
 DR EMBL; AF039943; AAB94767.1; -; mRNA.  
 DR HSP; P11749; 1H10.  
 DR SMR; OS7513; 3-121.  
 DR Ensembl; ENSGALG00000011620; Gallus gallus.



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DR InterPro: IPR000719; Prot kinase.
DR InterPro: IPR008271; Ser_thr_pkin_AS.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR InterPro: IPR001245; Tyr_pkinase.
DR Pfam: PF00169; PH; 1.
DR Pfam: PF00069; Pkinase; 1.
DR Pfam: PF00433; Pkinase C; 1.
DR ProDom: PD000001; Prot_kinase; 1.
DR SMART: SM00233; PH; 1.
DR SMART: SM00133; S_TK_X; 1.
DR SMART: SM00220; S_TK; 1.
DR SMART: SM00219; TyrKc; 1.
DR PROSITE: PS50003; PH DOMAIN; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
DR ATP-binding; Kinase; Nuclear protein; Nucleotide-binding;
KW Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 480 AA; 55748 MW; 152E6613C4E6D5A CRC64;

Query Match      89.3%; Score 1402.5; DB 2; Length 480;
Best Local Similarity 88.5%; Pred. No. 4.1e-85;
Matches 262; Conservative 19; Mismatches 14; Indels 1; Gaps 1;

QY 2 TNNDPDKLLKGGTGGKGVILVREKASGYKAMKILKEVIITAKDEVAHTLTESRVLKN 61
DB 146 TNNDPEYLLKLLGGTGGKGVILVREKATGRYAMKILKEVIIVAKDEVAHTLTENRVLQNS 205

QY 62 RHPFLTSLKYSFQTKDRLCFVMEYNGGELFPHLSRERVSFSDRTRFYGAIEVSALDYHL 121
DB 206 RHPFLTALKYSFQTHDRLCFVMEYANGGELFPHLSRERVSFSDRTRFYGAIEVSALDYHL 265

QY 122 SGK-IVYRDLENLMLDKGHKIKITDFGLCKEGITDAATMTKTCGTPPYLAPEVLEND 180
DB 266 SEKEVYVRDLLENLMLDKGHKIKITDFGLCKEGIKDGTATMTKTCGTPPYLAPEVLEND 325

QY 181 YGRAVDWGLGVVYEMMCGRLPFYVQNDHEKLFELILMEDIKFPRTLSDAKSLGLLI 240
DB 326 YGRAVDWGLGVVYEMMCGRLPFYVQNDHEKLFELILMEEIRFPRTLSPKASLGLLK 385

QY 241 KDPNKRLLGGPDDAKEIMRHSFFSGVNWQDVYDKLVPPFKQVTSSETDTRFYFDEE 296
DB 386 KDPKRLGGSGSEDAKEIMQRRFASIVQDVYVEKLLSPFPFKQVTSSETDTRFYFDEE 441

RESULT 12
ID Q4RLN6 TETNG PRELIMINARY; PRT; 1893 AA.
AC Q4RLN6;
DT 13-SEP-2005 (TReMBLrel. 31, Created)
DT 13-SEP-2005 (TReMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TReMBLrel. 31, Last annotation update)
DE Chromosome 10 SCAF15019, whole genome shotgun sequence.
DE (Fragment).
GN ORFNames=GSTENG00032408001;
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=99883;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Jaillon O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
RA Mauceli E., Bounie L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anthouard V., Jubin C., Castellani V., Katinka M., Vacherie B.,
RA Biemont C., Skalli Z., Cottolico L., Poulain J., De Berardinis V.,
RA Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Guzy J.,
RA Parra G., Lardier G., Chapple C., McKernan K.J., McEwan P., Bosak S.,
RA Kellis M., Volff J.N., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,

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RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA Winkler P., Lander E.S., Weissenbach J., Roest Crolius H.;
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RT the early vertebrate proto-karyotype.";
RL Nature 431:946-957(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RG Genoscope; Whitehead Institute Centre for Genome Research;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC -!- FUNCTION: Plays a key role in the control of the eukaryotic cell
CC cycle. It is required in higher cells for entry into S-phase and
CC mitosis. Component of the kinase complex that phosphorylates the
CC repetitive C-terminus of RNA polymerase II. Catalytic component of
CC MPF (By similarity).
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -!- SUBUNIT: Forms a stable but non-covalent complex with cyclin B in
CC mature oocytes (By similarity).
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
CC -!- SIMILARITY: Contains 1 PH domain.
DR EMBL: CAAB01015019; CAG10696.1; -; Genomic_DNA.
DR InterPro: IPR000253; PHA.
DR InterPro: IPR001849; PH.
DR InterPro: IPR000961; Pkinase C.
DR InterPro: IPR000719; Prot_kinase.
DR InterPro: IPR008271; Ser_thr_pkin_AS.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR InterPro: IPR001245; Tyr_pkinase.
DR Pfam: PF00498; PH; 1.
DR Pfam: PF00169; PH; 1.
DR Pfam: PF00069; Pkinase; 1.
DR Pfam: PF00433; Pkinase C; 1.
DR ProDom: PD000001; Prot_kinase; 1.
DR SMART: SM00240; PHA; 1.
DR SMART: SM00233; PH; 1.
DR SMART: SM00133; S_TK_X; 1.
DR SMART: SM00220; S_TK; 1.
DR SMART: SM00219; TyrKc; 1.
DR PROSITE: PS50006; PH DOMAIN; 1.
DR PROSITE: PS50003; PH DOMAIN; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
DR ATP-binding; Kinase; Nucleotide-binding;
KW Serine/threonine-protein kinase; Transferase.
FT NON_TER 1
FT NON_TER 1893
SQ SEQUENCE 1893 AA; 210868 MW; 7F9B5064C2BC2632 CRC64;

Query Match      89.3%; Score 1396.5; DB 2; Length 1893;
Best Local Similarity 87.2%; Pred. No. 4.6e-84;
Matches 258; Conservative 23; Mismatches 14; Indels 1; Gaps 1;

QY 2 TNNDPDKLLKGGTGGKGVILVREKASGYKAMKILKEVIITAKDEVAHTLTESRVLKN 61
DB 124 TNNDPEYLLKLLGGTGGKGVILVREKATGRYAMKILKEVIIVAKDEVAHTLTENRVLQNS 183

QY 62 RHPFLTSLKYSFQTKDRLCFVMEYNGGELFPHLSRERVSFSDRTRFYGAIEVSALDYHL 121
DB 184 RHPFLTGLKYSFQTHDRLCFVMEYANGGELFPHLSRERVSFSDRTRFYGAIEVSALDYHL 243

QY 122 SGK-IVYRDLENLMLDKGHKIKITDFGLCKEGITDAATMTKTCGTPPYLAPEVLEND 180
DB 244 AERNVYVRDLLENLMLDKGHKIKITDFGLCKEGIKDGTATMTKTCGTPPYLAPEVLEND 303

QY 181 YGRAVDWGLGVVYEMMCGRLPFYVQNDHEKLFELILMEDIKFPRTLSDAKSLGLLI 240
DB 304 YGRAVDWGLGVVYEMMCGRLPFYVQNDHEKLFELILMEDIRFPRTLSPKASLGLLK 363

QY 241 KDPNKRLLGGPDDAKEIMRHSFFSGVNWQDVYDKLVPPFKQVTSSETDTRFYFDEE 296
DB 386 KDPKRLGGSGSEDAKEIMQRRFASIVQDVYVEKLLSPFPFKQVTSSETDTRFYFDEE 441

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364 KDPWRLGGGPDDAKEIMQHFFAGIEWKDVYEKLVPPFPQVTSYDTRFYDDE 419

Db

## RESULT 13

AKT1\_RAT

DR PROSITE; PS0003; PH DOMAIN; 1.  
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.  
DR PROSITE; PS0011; PROTEIN\_KINASE\_DOM; 1.  
DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
KW ATP-binding; Kinase; Nucleotide-binding; Phosphorylation;  
KW Serine/threonine-protein kinase; Transferase.  
FT DOMAIN 5 108 PH.  
FT DOMAIN 150 408 Protein kinase.  
FT NP\_BIND 156 164 ATP (By similarity).  
FT ACT\_SITE 274 274 Proton acceptor (By similarity).  
FT BINDING 179 179 ATP (By similarity).  
FT MOD\_RES 308 308 Phosphothreonine (by PDPK1) (By similarity).  
FT MOD\_RES 473 473 Phosphoserine (by ILK1) (By similarity).  
FT MOD\_RES 474 474 Phosphotyrosine (By similarity).  
SQ SEQUENCE 480 AA; 55735 MW; 5DCAAE7134366D04 CRC64;  
Query Match 89.2%; Score 1394.5; DB 1; Length 480;  
Best Local Similarity 87.8%; Pred. No. 1.4e-84;  
Matches 260; Conservative 20; Mismatches 15; Indels 1; Gaps 1;  
Qy 2 TMNDFYLLKLGKGTGKVLVREKASGKYAMKILKEVIAKDEVAHILTSRLVNT 61  
Db 146 TMNEFEYLLKLGKGTGKVLVREKATGRYAMKILKEVIAKDEVAHILTSRLVNTS 205  
Qy 62 RHPFLTSKYSFOTKDLRCFVMEYVNGGELFFHLRSRVFSEDRTRFYGAIVSALDYH 121  
Db 206 RHPFLTSKYSFOTKDLRCFVMEYVNGGELFFHLRSRVFSEDRTRFYGAIVSALDYH 265  
Qy 122 SGK-IVYRDLEKLENLMDKDGHIKITDFGLCKEGITDAATMTKTCGTPYLAPEVLEND 180  
Db 266 SEKNVYVYRDLEKLENLMDKDGHIKITDFGLCKEGITDAATMTKTCGTPYLAPEVLEND 325  
Qy 181 YGRAVDWVGLGVVYEMMCGRLPFYNQDHKLELILMEIRPRTILGPEAKSLSLGLK 240  
Db 326 YGRAVDWVGLGVVYEMMCGRLPFYNQDHKLELILMEIRPRTILGPEAKSLSLGLK 385  
Qy 241 KDPNKLGGGPDDAKEIMQHFFAGIEWKDVYEKLVPPFPQVTSYDTRFYDDE 296  
Db 386 KDPNKLGGGPDDAKEIMQHFFAGIEWKDVYEKLVPPFPQVTSYDTRFYDDE 441  
RESULT 14  
Q6GSA6\_MOUSE  
ID Q6GSA6\_MOUSE PRELIMINARY; PRT; 480 AA.  
AC Q6GSA6\_MOUSE  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)  
DE Thymoma viral proto-oncogene 1 (protein kinase B-alpha).  
GN Name=Akt1;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muroidae; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6; TISSUE=Brain;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,  
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Boeak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";   
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6; TISSUE=Brain;  
RA Director MGC Project;  
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=129/SvJ;  
RX MEDLINE=22803305; PubMed=12783884; DOI=10.1074/jbc.M302847200;  
RA Yang Z.Z., Tschopp O., Hemmings-Mieszczak M., Feng J., Brodbeck D.,  
RA Perentes E., Hemmings B.A.;  
RT "Protein Kinase B(alpha)/Akt1 Regulates Placental Development and  
RT Fetal Growth.";   
RL J. Biol. Chem. 278:32124-32131 (2003).  
RN [4]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=129/SvJ;  
RA Yang Z., Hemmings B.A.;  
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.  
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.  
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.  
CC -!- SIMILARITY: Contains 1 PH domain.  
DR EMBL; AF534134; AAN04036.1; -; Genomic\_DNA.  
DR EMBL; BC66018; AAH66018.1; -; mRNA.  
DR SMR; QGSGA6; 3-121.  
DR Ensembl; ENSMUSG00000001729; Mus musculus.  
DR MGI; MGI:87986; Akt1.  
DR GO; GO:0005737; C:cytoplasm; IDA.  
DR GO; GO:0030027; C:lamellipodium; IDA.  
DR GO; GO:0005819; C:spindle; IDA.  
DR GO; GO:0005915; F:protein binding; IPI.  
DR GO; GO:0004672; F:protein kinase activity; IDA.  
DR GO; GO:0042640; P:anagen; IMP.  
DR GO; GO:0006915; P:apoptosis; IDA.  
DR GO; GO:0008637; P:apoptotic mitochondrial changes; IDA.  
DR GO; GO:0007281; P:germ cell development; IDA.  
DR GO; GO:0043066; P:negative regulation of apoptosis; IDA.  
DR GO; GO:0006468; P:protein amino acid phosphorylation; IDA.  
DR GO; GO:0030163; P:protein catabolism; IDA.  
DR GO; GO:0016567; P:protein ubiquitination; IDA.  
DR InterPro; IPR001849; PH.  
DR InterPro; IPR011993; PH type.  
DR InterPro; IPR000961; Pkinase C.  
DR InterPro; IPR000719; Prot\_kinase.  
DR InterPro; IPR008271; Ser\_thr\_pkin\_AS.  
DR InterPro; IPR002290; Ser\_thr\_pkinase.  
DR InterPro; IPR001245; Tyr\_pkinase.  
DR Pfam; PF00169; PH; 1.  
DR Pfam; PF00069; Pkinase; 1.  
DR Pfam; PF0433; Pkinase\_C; 1.  
DR SMART; SM00233; PH; 1.  
DR SMART; SM00133; S\_TK\_X; 1.  
DR SMART; SM00220; S\_TK; 1.  
DR SMART; SM00219; TyKc; 1.  
DR PROSITE; PS50003; PH\_DOMAIN; 1.  
DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.  
DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
KW ATP-binding; kinase; Nucleotide-binding;  
KW Serine/threonine-protein kinase; transferase.  
SQ SEQUENCE 480 AA; 55707 MW; 980DF2E5FE03730 CRC64;  
Query Match 89.2%; Score 1394.5; DB 2; Length 480;  
Best Local Similarity 87.8%; Pred. No. 14e-84;  
Matches 260; Conservative 20; Mismatches 15; Indels 1;  
Gaps 1;

QY 2 TANDDYLLKLGCTGFKVILVREKASGKYIYAKMLKKEVIAKDEVAHTLTESRVKVT 61  
DB 146 TMNEFEYLLKLGKGTGKGVILVREKATGRYYAMKILKKEVIAKDEVAHTLTENRVLQNS 205  
QY 62 RHPFLTSLKYSFQTKDRLCFVMEYVNGGELFPHLSRERVSFSDTRFRFYGAETVSALDYLLH 121  
DB 206 RHPFLTALKYSFQTHDRLCFVMEYANGGELFPHLSRERVSFSDRARFYGAETVSALDYLLH 265  
QY 122 SGK-IVYRDLEKLEMLDKOGHIKITDFGLCKEGITDAATMTKTCGTPPEYLAPEVLEDND 180  
DB 266 SEKNVYRDLKLEMLDKOGHIKITDFGLCKEGIKGATMTKTCGTPPEYLAPEVLEDND 325  
QY 181 YGRAVDWGLGVVYEMMCGRLPFYNQDHEKLFELILMEDIKFPRTLSLSDAKSLSLGLLI 240  
DB 326 YGRAVDWGLGVVYEMMCGRLPFYNQDHEKLFELILMEDIEIRFPRTLGEAKSLSLGLLK 385  
QY 241 KDPNKRLLGGPDDAKEIMRHSPFSGVNVQDVYDKLVPPFKQVTSSETDTRFYFDEE 296  
DB 386 KDPTQRLGGSEDAKEIMQHRRFFAIVNQDVYEKLSPPFKQVTSSETDTRFYFDEE 441

RESULT 15  
AKT\_MLVAT  
ID AKT\_MLVAT STANDARD; PRT; 501 AA.  
AC P31748;  
DT 01-JUL-1993 (Rel. 26, Created)  
DT 01-JUL-1993 (Rel. 26, Last sequence update)  
DT 13-SEP-2005 (Rel. 48, Last annotation update)  
DE AKT kinase transforming protein (EC 2.7.1.-).  
GN Name=V-AKT;  
OS AKT8 murine leukemia virus.  
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;  
OC Gammaretrovirus.  
OX NCBI\_TaxID=11790;  
RN [1]  
RP NUCLEOTIDE SEQUENCE [GENOMIC DNA].  
RX MEDLINE=92022574; PubMed=1833819;  
RA Bellacosa A., Testa J.R., Staal S.P., Tsichlis P.N.;  
RT "A retroviral oncogene, akt, encoding a serine-threonine kinase  
RT containing an SH2-like region.";   
RL Science 254:274-277 (1991).  
CC -!- PTM: Autophosphorylated on threonine and serine residues.  
CC -!- MISCELLANEOUS: This protein is synthesized as a Gag-Akt  
polyprotein.  
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family. RAC  
subfamily.  
CC -!- SIMILARITY: Contains 1 PH domain.  
CC This Swiss-Prot entry is copyright. It is produced through a collaboration  
between the Swiss Institute of Bioinformatics and the EMBL outstation -  
the European Bioinformatics Institute. There are no restrictions on its  
use as long as its content is in no way modified and this statement is not  
removed.  
DR EMBL; M80675; AAA42545.1; -; Genomic\_DNA.  
DR HSSP; P31749; 1H10.  
DR SMR; P31748; 24-142.  
DR InterPro; IPR001849; PH.  
DR InterPro; IPR011993; PH type.  
DR InterPro; IPR000961; Pkinase C.  
DR InterPro; IPR000719; Prot\_kinase.  
DR InterPro; IPR008271; Ser\_thr\_pkin\_AS.  
DR InterPro; IPR002290; Ser\_thr\_pkinase.  
DR Pfam; PF00169; PH; 1.  
DR Pfam; PF00069; Pkinase; 1.  
DR Pfam; PF0433; Pkinase\_C; 1.  
DR ProDom; PD000001; Prot\_kinase; 1.  
DR SMART; SM00233; PH; 1.  
DR SMART; SM00133; S\_TK\_X; 1.  
DR SMART; SM00220; S\_TK; 1.  
DR PROSITE; PS50003; PH\_DOMAIN; 1.  
DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.

DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
KW ATP-binding; Kinase; Nucleotide-Binding; Oncogene; Phosphorylation;  
KW Serine/threonine-protein kinase; Transferase.  
FT DOMAIN 26 129 PH.  
FT DOMAIN 171 429 Protein kinase.  
FT NP\_BIND 177 185 ATP (By similarity).  
FT ACT\_SITE 295 295 Proton acceptor (By similarity).  
FT BINDING 200 200 ATP (By similarity).  
FT MOD\_RES 347 347 Phosphotyrosine (By similarity).  
SQ SEQUENCE 501 AA; 57870 MW; 5AEFDE58CD42F773 CRC64;

Query Match 89.2%; Score 1394.5; DB 1; Length 501;  
Best Local Similarity 87.8%; Pred.No. 1.5e-84;  
Matches 260; Conservative 20; Mismatches 15; Indels 1; Gaps 1;

Qy 2 TMNDFYKLLGKGTFGKVIILVREKASGKYAMKILKKEVIAKDEVAHTLTESVLKNT 61  
Db 167 TMNEFEYKLLGKGTFGKVIILVREKATGRYAMKILKKEVIAKDEVAHTLTENRVLQNS 226  
Qy 62 RHPFLTSLKYSFQTKDRLCFVMEYVNGGELFFHLSRERVSEDRTRFYGAIVSALDYH 121  
Db 227 RHPFLTALKYSFQTHDRLCFVMEYANGGELFFHLSRERVSEDRARFYGAIVSALDYH 286  
Qy 122 SGK-IVYRDLKLENMLDKGHIKITDFGLCKEGITDAATMKTCGTPGYLAPEVLEDND 180  
Db 287 SEKNVYRDLKLENMLDKGHIKITDFGLCKEGIKDGTWKTCGTPGYLAPEVLEDND 346  
Qy 181 YGRAVDWGLGVVYEMMCGRLPFYNQDHEKLFELLIMEDIKFPRTLSDDAKSLLSGLLI 240  
Db 347 YGRAVDWGLGVVYEMMCGRLPFYNQDHEKLFELLIMEEIRFPRTLGPAAKSLLSGLLK 406  
Qy 241 KDPNKRLLGGGPDDAKEIMRHSFFSGVNWQDVYDKLVPPPKPQVTSSTDTRYFDEE 296  
Db 407 KDPTQRLGGGSEDAKEIMQHRFFANIVWQDVYEKLSPPFPKPQVTSSTDTRYFDEE 462

Search completed: February 13, 2006, 06:40:49  
Job time : 429 secs

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on: February 13, 2006, 06:33:54 ; Search time 73 Seconds  
(without alignments)  
390.139 Million cell updates/sec

Title: US-10-601-311-1\_COPY\_143\_438

Perfect score: 1563

Sequence: 1 KTMNDFYLLKLGKTFGKV.....VPPFPQVTSYDTRFYDEE 296

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 80:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1563	100.0	462	1 T17287	protein kinase (EC
2	1563	100.0	479	1 A59380	protein kinase (EC
3	1558	99.7	454	1 JC4345	protein kinase (EC
4	1394.5	89.2	480	1 JC2437	protein kinase (EC
5	1394.5	89.2	480	1 S33364	protein kinase (EC
6	1394.5	89.2	763	1 A40831	gag-akt polyprot
7	1393.5	89.2	480	1 A39360	protein kinase (EC
8	1391	89.0	481	1 A46288	protein kinase (EC
9	1378.5	88.2	480	1 S62117	protein kinase (EC
10	1378	88.2	481	1 JC2438	protein kinase (EC
11	1240	79.3	611	1 A55888	protein kinase (EC
12	1118.5	71.6	546	1 T43233	protein kinase (EC
13	1098	70.2	541	1 T43232	protein kinase (EC
14	1032	66.0	528	1 T21523	protein kinase (EC
15	1027	65.7	483	1 T43234	protein kinase (EC
16	857	54.8	431	2 A48094	serum and glucoc
17	826	52.8	683	1 A23690	protein kinase (EC
18	822	52.6	683	1 S29478	protein kinase C
19	819.5	52.4	736	1 KIRBCE	protein kinase C
20	819.5	52.4	737	1 KINSC2	protein kinase C
21	819.5	52.4	737	1 S28942	protein kinase C
22	819	52.4	1016	1 A46079	protein kinase C
23	815	52.1	682	1 A39666	protein kinase C
24	811.5	51.9	737	1 KIRTC2	protein kinase C
25	811	51.9	1096	1 S61917	protein kinase C
26	807	51.6	1174	2 T43051	protein kinase C
27	802	51.3	988	1 S35362	protein kinase C
28	800.5	51.2	547	2 T22856	hypothetical prote
29	799.5	51.2	671	1 KIHUC1	protein kinase C

30	798	51.1	634	1 B32392	protein kinase C
31	797.5	51.0	671	1 KIRBC1	protein kinase C
32	797.5	51.0	707	1 A53530	protein kinase C
33	796.5	51.0	671	1 KIRTC1	protein kinase C
34	796	50.9	1139	1 S61918	protein kinase C
35	793	50.7	1102	2 T28666	protein kinase C-r
36	782	50.0	680	2 S37955	protein kinase YPK
37	779	49.8	672	1 KIBOC	protein kinase C
38	779	49.8	673	1 KIBOC2	protein kinase C
39	779	49.8	673	1 KIHUC2	protein kinase C
40	779	49.8	673	2 S11213	protein kinase C
41	778	49.8	422	2 T26334	hypothetical prote
42	778	49.8	672	1 KIRBC	protein kinase C
43	777.5	49.7	479	2 A38578	protein kinase 2
44	777	49.7	672	1 KIHUCA	protein kinase C
45	777	49.7	672	1 KIMSCA	protein kinase C

ALIGNMENTS

RESULT 1

T17287

protein kinase (EC 2.7.1.37) akt3 short splice form - human

N:Alternate names: protein kinase B gamma; RAC-PK-gamma; serine/threonine-specific protei

C:Species: Homo sapiens (man)

C>Date: 31-Mar-2001 #sequence\_revision 31-Mar-2001 #text\_change 16-Aug-2004

C:Accession: T17287

R:Poustka, A.; Klein, M.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.

submitted to the Protein Sequence Database, September 1999

A:Reference number: Z18723

A:Accession: T17287

A:Molecule type: mRNA

A:Residues: 1-462 <POU>

A:Cross-references: UNIPARC:UPI000016AC77; EMBL:AL117525; GB:CAB55977; NID:G5912043; PIDN

A:Experimental source: adult testis; clone DKFZp434N0250

R:Nakatani, K.; Thompson, D.A.; Barthel, A.; Sakaue, H.; Liu, W.; Weigel, R.J.; Roth, R.J

J. Biol. Chem. 274, 21528-21532, 1999

A:Title: Up-regulation of Akt3 in estrogen receptor-deficient breast cancers and amdrpgen

A:Reference number: A64199; PMID:10419456

A:Contents: annotation

C:Comment: This protein is increased in estrogen receptor-negative breast cancers and an

C:Genetics:

A:Gene: GDB:AKT3

A:Cross-references: GDB:9954867

A:Map position: lq44-lq44

C:Function:

A:Pathway: signal transduction pathways regulating various processes

C:Superfamily: RAC serine/threonine-protein kinase; pleckstrin repeat homology; protein k

C:Keywords: ATP; phosphoprotein; phosphotransferase; serine/threonine-specific protein k

F:4-105/Domain: pleckstrin repeat homology <PLK>

F:146-405/Domain: protein kinase homology <KIN>

F:154-162/Region: protein kinase ATP-binding motif

F:177/Active site: Lys #status predicted

Query Match 100.0%; Score 1563; DB 1; Length 462;

Best Local Similarity 100.0%; Pred. No. 1e-63;

Matches 296; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	KTMNDFYLLKLGKTFGKVILVREKASGKYAMKILKEVIAKDEVAAHTLTESVLKN	60
Db	143	KTMNDFYLLKLGKTFGKVILVREKASGKYAMKILKEVIAKDEVAAHTLTESVLKN	202
Qy	61	TRHPFLTSLKYSFQTKDRLCFVMEYVNGGELFFHLRSRVFSDTRFPGAEIVSALDYL	120
Db	203	TRHPFLTSLKYSFQTKDRLCFVMEYVNGGELFFHLRSRVFSDTRFPGAEIVSALDYL	262
Qy	121	HSGKIVYRDLKLENLMDKDGHIKITDFGLCKEGITDAATMTKTCGTPRYLAPEVLND	180
Db	263	HSGKIVYRDLKLENLMDKDGHIKITDFGLCKEGITDAATMTKTCGTPRYLAPEVLND	322
Qy	181	YGRADVWVGWGLGVVYEMMCGRLPFFYNQDHEKLFELILMEDIKFPPTLSDDAKSLLSGLLI	240

Db 323 YGRAVDWMLGVVYEMMCGSLFPYNDQHEKLFELLIMEDIKFPRTLSSDAKSLLSGLLI 382  
Qy 241 KDPNKRLLGGGDDDAKEIMRHSHFFSGVNWQDVYDKLVPPPKPQVTSSTDTRYFDEE 296  
Db 383 KDPNKRLLGGGDDDAKEIMRHSHFFSGVNWQDVYDKLVPPPKPQVTSSTDTRYFDEE 438

RESULT 2  
A59380  
protein kinase (EC 2.7.1.37) akt3 long splice form [similarity] - human  
N;Alternate names: protein kinase B gamma; RAC-pK-gamma; serine/threonine-specific protei  
C;Species: Homo sapiens (man)  
C;Date: 31-Mar-2001 #sequence\_revision 31-Mar-2001 #text\_change 16-Aug-2004  
C;Accession: A59380; MUID:99194749; PMID:10092583  
R;Brodebeck, D.; Cron, P.; Hammings, B.A.  
J. Biol. Chem. 274, 9133-9136, 1999  
A;Title: A human protein kinase Bgamma with regulatory phosphorylation sites in the acti  
A;Reference number: A59380; MUID:99194749; PMID:10092583  
A;Accession: A59380  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-479 <BRO>  
A;Cross-references: UNIPROT:Q9Y243; UNIPARC:UPI00000335E8; GB:AD29089; NID:94757579; PI  
R;Maure, S.; Haefner, B.; Wesselink, J.J.; Hoefnagel, E.; Mortier, E.; Verhaaselt, P.;  
Eur. J. Biochem. 265, 353-360, 1999  
A;Title: Molecular cloning, expression and characterization of the human serine/threonin  
A;Reference number: A59379; MUID:99421751; PMID:10491192  
A;Accession: A59379  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-479 <MAS>  
A;Cross-references: UNIPARC:UPI00000335E8; GB:CAB53537; NID:95804886; PIDN:CAB53537.1  
C;Genetics:  
A;Gene: GDB:AKT3; PK3G; PRK3G; RAC-gamma  
A;Cross-references: GDB:9954867  
A;Map position: lq44-lq44  
C;Function:  
A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin  
A;Pathway: signal transduction pathways regulating various processes  
C;Superfamily: RAC serine/threonine-protein kinase; pleckstrin repeat homology; protein  
C;Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; proto-oncogene  
F;7-108/Domain: pleckstrin repeat homology <PK>  
F;149-408/Domain: protein kinase homology <PK>  
F;157-165/Region: protein kinase ATP-binding motif  
F;177/Active site: Lys #status predicted  
F;305/Binding site: phosphate (Thr) (covalent) #status predicted  
F;474/Binding site: phosphate (Ser) (covalent) (by autophosphorylation) #status predicte

Query Match 100.0%; Score 1563; DB 1; Length 479;  
Best Local Similarity 100.0%; Pred. No. 1.le-63;  
Matches 296; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KTNMDFYLLKLGKGTGKVLVREKASGKYAMKILKKEVIIAKDEVAHTLTSRVLKN 60  
Db 143 KTNMDFYLLKLGKGTGKVLVREKASGKYAMKILKKEVIIAKDEVAHTLTSRVLKN 202

Qy 61 TRHPFLTSLKYSFQTKDRLCFVMEYVNGGELFFHLRSRVSFSDRTFRFYGAIEVSALDYL 120  
Db 203 TRHPFLTSLKYSFQTKDRLCFVMEYVNGGELFFHLRSRVSFSDRTFRFYGAIEVSALDYL 262

Qy 121 HSGKIVYRDLKLENLMDKDGHKITDFGLCKEGITDAATWKTFCGTPEYLAPEVLEND 180  
Db 263 HSGKIVYRDLKLENLMDKDGHKITDFGLCKEGITDAATWKTFCGTPEYLAPEVLEND 322

Qy 181 YGRAVDWMLGVVYEMMCGRLFPYNQDHEKLFELLIMEDIKFPRTLSSDAKSLLSGLLI 240  
Db 323 YGRAVDWMLGVVYEMMCGRLFPYNQDHEKLFELLIMEDIKFPRTLSSDAKSLLSGLLI 382

Query Match 100.0%; Score 1563; DB 1; Length 479;  
Best Local Similarity 100.0%; Pred. No. 1.le-63;  
Matches 296; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KTNMDFYLLKLGKGTGKVLVREKASGKYAMKILKKEVIIAKDEVAHTLTSRVLKN 60  
Db 143 KTNMDFYLLKLGKGTGKVLVREKASGKYAMKILKKEVIIAKDEVAHTLTSRVLKN 202

Qy 61 TRHPFLTSLKYSFQTKDRLCFVMEYVNGGELFFHLRSRVSFSDRTFRFYGAIEVSALDYL 120  
Db 203 TRHPFLTSLKYSFQTKDRLCFVMEYVNGGELFFHLRSRVSFSDRTFRFYGAIEVSALDYL 262

Qy 121 HSGKIVYRDLKLENLMDKDGHKITDFGLCKEGITDAATWKTFCGTPEYLAPEVLEND 180  
Db 263 HSGKIVYRDLKLENLMDKDGHKITDFGLCKEGITDAATWKTFCGTPEYLAPEVLEND 322

Qy 181 YGRAVDWMLGVVYEMMCGRLFPYNQDHEKLFELLIMEDIKFPRTLSSDAKSLLSGLLI 240  
Db 323 YGRAVDWMLGVVYEMMCGRLFPYNQDHEKLFELLIMEDIKFPRTLSSDAKSLLSGLLI 382

Qy 241 KDPNKRLLGGGDDDAKEIMRHSHFFSGVNWQDVYDKLVPPPKPQVTSSTDTRYFDEE 296  
Db 383 KDPNKRLLGGGDDDAKEIMRHSHFFSGVNWQDVYDKLVPPPKPQVTSSTDTRYFDEE 438

RESULT 3  
JC4345  
protein kinase (EC 2.7.1.37) akt3 [validated] - rat  
N;Alternate names: protein kinase B gamma; RAC-pK-gamma; serine/threonine-specific protei  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 31-Mar-2001 #sequence\_revision 31-Mar-2001 #text\_change 16-Aug-2004  
C;Accession: JC4345  
R;Konishi, H.; Kuroda, S.; Tanaka, M.; Matsuzaki, H.; Ono, Y.; Kameyama, K.; Haga, T.; Ki  
Biochem. Biophys. Res. Commun. 216, 526-534, 1995  
A;Title: Molecular cloning and characterization of a new member of the RAC protein kinase  
e C subtypes and beta gamma subunits of G proteins.  
A;Reference number: JC4345; MUID:96063640; PMID:7488143  
A;Accession: JC4345  
A;Molecule type: mRNA  
A;Residues: 1-454 <KON>  
A;Cross-references: UNIPROT:Q63484; UNIPARC:UPI000012577F; DBBJ:D49836; NID:g1136777; PII  
A;Experimental source: brain  
C;Function:  
A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonine  
A;Pathway: signal transduction pathways regulating various processes  
C;Superfamily: RAC serine/threonine-protein kinase; pleckstrin repeat homology; protein  
C;Keywords: ATP; phosphoprotein; phosphotransferase; serine/threonine-specific protein k  
F;4-105/Domain: pleckstrin repeat homology <PLK>  
F;146-405/Domain: protein kinase homology <KIN>  
F;154-162/Region: protein kinase ATP-binding motif  
F;177/Active site: Lys #status predicted

Query Match 99.7%; Score 1558; DB 1; Length 454;  
Best Local Similarity 99.7%; Pred. No. 1.7e-63;  
Matches 295; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KTNMDFYLLKLGKGTGKVLVREKASGKYAMKILKKEVIIAKDEVAHTLTSRVLKN 60  
Db 143 KTNMDFYLLKLGKGTGKVLVREKASGKYAMKILKKEVIIAKDEVAHTLTSRVLKN 202

Qy 61 TRHPFLTSLKYSFQTKDRLCFVMEYVNGGELFFHLRSRVSFSDRTFRFYGAIEVSALDYL 120  
Db 203 TRHPFLTSLKYSFQTKDRLCFVMEYVNGGELFFHLRSRVSFSDRTFRFYGAIEVSALDYL 262

Qy 121 HSGKIVYRDLKLENLMDKDGHKITDFGLCKEGITDAATWKTFCGTPEYLAPEVLEND 180  
Db 263 HSGKIVYRDLKLENLMDKDGHKITDFGLCKEGITDAATWKTFCGTPEYLAPEVLEND 322

Qy 181 YGRAVDWMLGVVYEMMCGRLFPYNQDHEKLFELLIMEDIKFPRTLSSDAKSLLSGLLI 240  
Db 323 YGRAVDWMLGVVYEMMCGRLFPYNQDHEKLFELLIMEDIKFPRTLSSDAKSLLSGLLI 382

Qy 241 KDPNKRLLGGGDDDAKEIMRHSHFFSGVNWQDVYDKLVPPPKPQVTSSTDTRYFDEE 296  
Db 383 KDPNKRLLGGGDDDAKEIMRHSHFFSGVNWQDVYDKLVPPPKPQVTSSTDTRYFDEE 438

RESULT 4  
JC2437  
protein kinase (EC 2.7.1.37) akt1 [validated] - rat  
N;Alternate names: protein kinase B alpha; RAC-pK-alpha; serine/threonine-specific protei  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 31-Mar-2001 #sequence\_revision 31-Mar-2001 #text\_change 16-Aug-2004  
C;Accession: JC2437  
R;Konishi, H.; Shinomura, T.; Kuroda, S.; Ono, Y.; Kikkawa, U.  
Biochem. Biophys. Res. Commun. 205, 817-825, 1994  
A;Title: Molecular cloning of rat RAC protein kinase alpha and beta and their associatio  
A;Reference number: JC2437; MUID:95091823; PMID:7999118  
A;Accession: JC2437  
A;Molecule type: mRNA  
A;Residues: 1-480 <KON>  
A;Cross-references: UNIPROT:P47196; UNIPARC:UPI000012E044; DBBJ:D30040; NID:g485402; PDI  
A;Experimental source: testis  
C;Function:  
A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonine  
A;Pathway: signal transduction pathways regulating various processes  
C;Superfamily: RAC serine/threonine-protein kinase; pleckstrin repeat homology; protein



C:Keywords: ATP; autophosphorylation; phosphoprotein; phosphoprotein; phosphotransferase; proto-oncogene  
F:4-106/Domain: pleckstrin repeat homology <PK>  
F:148-408/Domain: protein kinase homology <KIN>  
F:156-164/Region: protein kinase ATP-binding motif  
F:179/Active site: Lys #status predicted  
F:308/Binding site: phosphate (Thr) (covalent) (by autophosphorylation) #status predicted  
F:473/Binding site: phosphate (Ser) (covalent) (by autophosphorylation) #status predicted

Query Match 89.2%; Score 1394.5; DB 1; Length 480;  
Best Local Similarity 87.8%; Pred. No. 3.8e-56;  
Matches 260; Conservative 20; Mismatches 15; Indels 1; Gaps 1;

Qy 2 TWNDFYLLKLGKGFVGVVREKASGYAMKILKKEVIAKDEVAHTLTESRLKNT 61  
Db 146 TWNEFYLLKLGKGFVGVVREKATGYAMKILKKEVIAKDEVAHTLTENRVLQNS 205

Qy 62 RHPFLTSLKYSFQTKDRLCFVMEYVNGGELFPHLSRERVFSEDRTRFYGAIEVSALDYIH 121  
Db 206 RHPFLTALKYSFQTHDRLCFVMEYANGGELFPHLSRERVFSEDRARFYGAIEVSALDYIH 265

Qy 122 SGK-IVYRDLEKLEMLDKDGHIKITDFGLCKEGITDAATMKTFCGTPEYLAPEVLEND 180  
Db 266 SEKNNVYRDLEKLEMLDKDGHIKITDFGLCKEGIKDGTATMKTFCGTPEYLAPEVLEND 325

Qy 191 YGRAVDWGLGVVMEYVNGGELFPHLSRERVFSEDRTRFYGAIEVSALDYIH 240  
Db 326 YGRAVDWGLGVVMEYVNGGELFPHLSRERVFSEDRARFYGAIEVSALDYIH 385

Qy 241 KDPNKRLLGGGPDDAKEIMRHSFSGVNVQDVYDKLVPPFPQVTSSETDTRYFDEE 296  
Db 386 KDPTQRLGGSEDAKEIMQHRFFANIVWQDVYEKKLSPFPKPQVTSSETDTRYFDEE 441

RESULT 5

S33364  
N:Alternate names: protein kinase B alpha; RAC-PK-alpha; serine/threonine-specific prote  
C:Species: Mus musculus (house mouse)  
C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 16-Aug-2004  
C:Accession: S33364  
R:Bellacosa, A.; Franke, T.F.; Gonzalez-Portal, M.E.; Datta, K.; Taguchi, T.; Gardner, J  
Oncogene 8, 745-754, 1993  
A:Title: Structure, expression and chromosomal mapping of c-akt: relationship to v-akt a  
A:Reference number: S33364; MUID:93173519; PMID:8437858  
A:Accession: S33364  
A:Status: preliminary  
A:Gene: MGI:Akt  
A:Molecule type: mRNA  
A:Residues: 1-480 <BEL>  
A:Cross-references: UNIPROT:P31750; UNIPARC:UPI0000001726; EMBL:X65687; NID:g287806; PID  
C:Genetics:  
A:Gene: MGI:Akt  
A:Cross-references: MGI:87986  
A:Map position: 12  
C:Function:  
A:Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin  
A:Pathway: signal transduction pathways regulating various processes  
C:Superfamily: RAC serine/threonine-protein kinase; pleckstrin repeat  
C:Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; proto-oncogene  
F:4-106/Domain: pleckstrin repeat homology <PK>  
F:148-408/Domain: protein kinase homology <KIN>  
F:156-164/Region: protein kinase ATP-binding motif  
F:179/Active site: Lys #status predicted  
F:308/Binding site: phosphate (Thr) (covalent) (by phosphoinositide-dependent protein ki  
F:473/Binding site: phosphate (Ser) (covalent) (by autophosphorylation) #status predicted

Query Match 89.2%; Score 1394.5; DB 1; Length 480;  
Best Local Similarity 87.8%; Pred. No. 3.8e-56;  
Matches 260; Conservative 20; Mismatches 15; Indels 1; Gaps 1;

Qy 2 TWNDFYLLKLGKGFVGVVREKASGYAMKILKKEVIAKDEVAHTLTESRLKNT 61  
Db 146 TWNEFYLLKLGKGFVGVVREKATGYAMKILKKEVIAKDEVAHTLTENRVLQNS 205

Qy 62 RHPFLTSLKYSFQTKDRLCFVMEYVNGGELFPHLSRERVFSEDRTRFYGAIEVSALDYIH 121  
Db 206 RHPFLTALKYSFQTHDRLCFVMEYANGGELFPHLSRERVFSEDRARFYGAIEVSALDYIH 265

Qy 122 SGK-IVYRDLEKLEMLDKDGHIKITDFGLCKEGITDAATMKTFCGTPEYLAPEVLEND 180  
Db 266 SEKNNVYRDLEKLEMLDKDGHIKITDFGLCKEGIKDGTATMKTFCGTPEYLAPEVLEND 325

Qy 191 YGRAVDWGLGVVMEYVNGGELFPHLSRERVFSEDRTRFYGAIEVSALDYIH 240  
Db 326 YGRAVDWGLGVVMEYVNGGELFPHLSRERVFSEDRARFYGAIEVSALDYIH 385

Qy 241 KDPNKRLLGGGPDDAKEIMRHSFSGVNVQDVYDKLVPPFPQVTSSETDTRYFDEE 296  
Db 386 KDPTQRLGGSEDAKEIMQHRFFANIVWQDVYEKKLSPFPKPQVTSSETDTRYFDEE 441

RESULT 6

A40831  
gag-akt polyprotein - AKT8 murine leukemia virus  
N:Contains: amino end of core protein p30; core protein p15; inner coat protein p12; kin  
C:Species: AKT8 murine leukemia virus  
C:Date: 12-Feb-1993 #sequence\_revision 12-May-1994 #text\_change 31-Dec-2004  
C:Accession: A40831; B40831  
R:Bellacosa, A.; Testa, J.R.; Staal, S.P.; Tsichlis, P.N.  
Science 254, 274-277, 1991  
A:Title: A retroviral oncogene, akt, encoding a serine-threonine kinase containing an SH  
A:Reference number: A40831; MUID:9202574; PMID:1833819  
A:Accession: A40831  
A:Molecule type: DNA  
A:Residues: 1-262 <BEL>  
A:Cross-references: UNIPARC:UPI000001725AF; GB:M80675  
A:Accession: B40831  
A:Molecule type: DNA  
A:Residues: 262-763 <BE2>  
A:Cross-references: UNIPARC:UPI000001725B0; GB:M80675  
C:Genetics:  
A:Gene: gag-akt  
C:Keywords: ATP; core protein; glycoprotein; oncogene; phosphoprotein; phosphotransferase  
F:1-129/Product: core protein p15 #status predicted <CP1>  
F:130-214/Product: inner coat protein p12 #status predicted <CP2>  
F:284-763/Product: kinase-related transforming protein akt #status predicted <AKT>  
F:287-389/Domain: pleckstrin repeat homology <PLK>  
F:431-691/Domain: protein kinase homology <KIN>  
F:439-447/Region: protein kinase ATP-binding motif  
F:25.337/Binding site: carboxylate (Asn) (covalent) #status predicted  
F:462/Active site: Lys #status predicted  
F:509/Binding site: phosphate (Tyr) (covalent) #status predicted

Query Match 89.2%; Score 1394.5; DB 1; Length 763;  
Best Local Similarity 87.8%; Pred. No. 5.5e-56;  
Matches 260; Conservative 20; Mismatches 15; Indels 1; Gaps 1;

Qy 2 TWNDFYLLKLGKGFVGVVREKASGYAMKILKKEVIAKDEVAHTLTESRLKNT 61  
Db 429 TWNEFYLLKLGKGFVGVVREKATGYAMKILKKEVIAKDEVAHTLTENRVLQNS 488

Qy 62 RHPFLTSLKYSFQTKDRLCFVMEYVNGGELFPHLSRERVFSEDRTRFYGAIEVSALDYIH 121  
Db 489 RHPFLTALKYSFQTHDRLCFVMEYANGGELFPHLSRERVFSEDRARFYGAIEVSALDYIH 548

Qy 122 SGK-IVYRDLEKLEMLDKDGHIKITDFGLCKEGITDAATMKTFCGTPEYLAPEVLEND 180  
Db 549 SEKNNVYRDLEKLEMLDKDGHIKITDFGLCKEGIKDGTATMKTFCGTPEYLAPEVLEND 608

Qy 191 YGRAVDWGLGVVMEYVNGGELFPHLSRERVFSEDRTRFYGAIEVSALDYIH 240  
Db 609 YGRAVDWGLGVVMEYVNGGELFPHLSRERVFSEDRARFYGAIEVSALDYIH 668

Qy 241 KDPNKRLLGGGPDDAKEIMRHSFSGVNVQDVYDKLVPPFPQVTSSETDTRYFDEE 296  
Db 669 KDPTQRLGGSEDAKEIMQHRFFANIVWQDVYEKKLSPFPKPQVTSSETDTRYFDEE 724

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RESULT 7
A39360
Protein kinase (EC 2.7.1.37) akt1 [validated] - human
N;Alternate names: protein kinase B alpha; RAC-PK-alpha; serine/threonine-specific prote
C;Species: Homo sapiens (man)
C;Date: 20-Mar-1992 #sequence_revision 12-May-1994 #text_change 16-Aug-2004
C;Accession: A39360; S36389; S18000; S20836
R;Jones, P.F.; Jakubowicz, T.; Picossi, F.J.; Maurer, F.; Hemmings, B.A.
Proc. Natl. Acad. Sci. U.S.A. 88, 4171-4175, 1991
A;Title: Molecular cloning and identification of a serine/threonine protein kinase of th
A;Reference number: A39360; MUID:91239529; PMID:1851997
A;Accession: A39360
A;Molecule type: mRNA
A;Residues: 1-480 <JON>
A;Cross-references: UNIPROT:P31749; UNIPARC:UPI000002E75B; GB:M63167; NID:g190827; PIDN:
R;Coffer, P.J.; Woodgett, J.R.
Eur. J. Biochem. 205, 1217, 1992
A;Reference number: S24423; MUID:92249329; PMID:1533586
A;Contents: erratum
A;Accession: S36389
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: mRNA
A;Residues: 63-172, 'A', 175-201, 'Q', 203-211, 'R', 213-245, 'A', 247-408, 'T', 410-475, 'P', 477, '
A;Cross-references: UNIPARC:UPI000016AEB1; EMBL:X61037; NID:G35480; PIDN:CAA43372.1; PID
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, December 1991
A;Note: this a revision to the sequence from reference S17999
R;Coffer, P.J.; Woodgett, J.R.
Eur. J. Biochem. 201, 475-481, 1991
A;Title: Molecular cloning and characterisation of a novel putative protein-serine kinase
A;Reference number: S17999; MUID:92037600; PMID:1718748
A;Accession: S18000
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 63-70, 'TPSSSAACGPISSNAPSWMRLRSGVDNRHPDCGRRPQ', 'EAGGGDGLPVGLTORQLRGRDRGGV
A;Cross-references: UNIPARC:UPI00001725AC; EMBL:X61037
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1991
A;Note: this sequence has been revised in reference S24423
R;Coffer, P.
submitted to the EMBL Data Library, July 1991
A;Reference number: S20836
A;Accession: S20836
A;Molecule type: mRNA
A;Residues: 63-70, 'TPSSSAACGPISSNAPSWMRLRSGVDNRHPDCGRRPQ', 'EAGGGDGLPVGLTORQLRGRDRGGV
A;Cross-references: UNIPARC:UPI00001725AC; EMBL:X61037
A;Note: this sequence has been revised in reference S24423
R;Alessi, D.R.; Andjelkovic, M.; Caudwell, B.; Cron, P.; Morrice, N.; Cohen, P.; Hemming
EMBO J. 15, 6541-6551, 1996
A;Title: Mechanism of activation of protein kinase B by insulin and IGF-1.
A;Reference number: A64192; MUID:97133284; PMID:8978681
A;Contents: annotation; phosphorylation sites
R;Toker, A.; Newton, A.C.
J. Biol. Chem. 275, 8271-8274, 2000
A;Title: Akt/protein kinase B is regulated by autophosphorylation at the hypothetical PI
A;Reference number: A64193; MUID:20187529; PMID:10722653
A;Contents: annotation; autophosphorylation site
C;Comment: Akt1 is ubiquitous as an inactive multimeric complex. It binds phosphatidy-3
nt protein kinase 1 complex. Akt1 can then autophosphorylate and become fully active.
C;Genetics:
A;Gene: GDB:AKT1; RAC; PKB
A;Cross-references: GDB:118989; OMIM:164730
A;Map position: 14q32.32-14q32.32
C;Function:
A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonin
e production
A;Pathway: signal transduction pathways regulating various processes including insulin a
C;Superfamily: RAC serine/threonine-protein kinase; pleckstrin repeat homology; protein
C;Keywords: ATP; autophosphorylation; phosphoprotein; phosphotransferase; proto-oncogene
F;4-106/Domain: pleckstrin repeat homology <PLK>
F;148-408/Domain: protein kinase homology <KIN>
F;156-164/Region: protein kinase ATP-binding motif
F;179/Active site: Lys #status predicted
F;308/Binding site: phosphate (Thr) (covalent) (by phosphoinositide-dependent protein ki

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F;473/Binding site: phosphate (Ser) (covalent) (by autophosphorylation) #status experimer

Query Match      89.2%; Score 1393.5; DB 1; Length 480;
Best Local Similarity 87.8%; Pred. No. 4.2e-56;
Matches 260; Conservative 20; Mismatches 15; Indels 1; Gaps 1;

QY 2 TMNDFDYLLKLGKGTGKGVILVREKASGKYAMKILKKEVIAKDEVAHTLTESRLVKNT 61
DB 146 TMNEFEVLLKLGKGTGKGVILVREKATGRYYAMKILKKEVIAKDEVAHTLTENRVLQNS 205

QY 62 RHPFLTSLKYSFQTKDRLCFVMEYVNGGELFFHLSRERVFSEDRTRFYGAIVSALDYHL 121
DB 206 RHPFLTALKYSFQTHDRLCFVMEYANGGELFFHLSRERVFSEDRARFYGAIVSALDYHL 265

QY 122 SGK-IYVRDLKLENMLDKDGHKITDPGLCKEGITDAATMKTFCGTPEYLAPEVLEND 180
DB 266 SERNVVTRDKLENMLDKDGHKITDFGLCKEGIKDGMKTFCGTPEYLAPEVLEND 325

QY 181 YGRAVDWMLGVVMEYEMMCGRLPFYVQDHEKLFELILMEDIKFPRTLSDDAKSLLSGLLI 240
DB 326 YGRAVDWMLGVVMEYEMMCGRLPFYVQDHEKLFELILMEIRFPTLGPPEAKSLLSGLLK 385

QY 241 KDNKRLGGGPDDAKEIMRHSFSGVNMVDVYDKLVPPFPKQVTSQTDTRYFDEE 296
DB 386 KDPKQRLGGGSEDAKEIMQHRFFAGIYVQHVYKSLSPFPKQVTSQTDTRYFDEE 441

RESULT 8
A46288
protein kinase (EC 2.7.1.37) akt2 - human
N;Alternate names: protein kinase B beta; RAC-PK-beta; serine/threonine-specific protein
C;Species: Homo sapiens (man)
C;Date: 22-Sep-1993 #sequence_revision 12-May-1994 #text_change 16-Aug-2004
C;Accession: A46288
R;Cheng, J.Q.; Godwin, A.K.; Bellacosa, A.; Taguchi, T.; Franke, T.F.; Hamilton, T.C.; Te
Proc. Natl. Acad. Sci. U.S.A. 89, 9267-9271, 1992
A;Title: AKT2, a putative oncogene encoding a member of a subfamily of protein-serine/thr
A;Reference number: A46288; MUID:93028445; PMID:1409633
A;Accession: A46288
A;Molecule type: mRNA
A;Residues: 1-481 <CHE>
A;Cross-references: UNIPROT:P31751; UNIPARC:UPI0000049EDB; GB:M95936; NID:g178325; PIDN:
A;Note: sequence extracted from NCBI backbone (NCBI:P:115859)
C;Comment: This protein is amplified in some pancreatic, ovarian, and other carcinomas.
C;Genetics:
A;Gene: GDB:AKT2
A;Cross-references: GDB:1135660; OMIM:164731
A;Map position: 19q13.2-19q13.2
C;Function:
A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonine
C;Pathway: signal transduction pathways regulating various processes
C;Superfamily: RAC serine/threonine-protein kinase; pleckstrin repeat homology; protein
C;Keywords: ATP; phosphoprotein; phosphotransferase; serine/threonine-specific protein k
F;4-106/Domain: pleckstrin repeat homology <PLK>
F;150-409/Domain: protein kinase homology <KIN>
F;158-166/Region: protein kinase ATP-binding motif
F;181/Active site: Lys #status predicted

Query Match      89.0%; Score 1391; DB 1; Length 481;
Best Local Similarity 86.4%; Pred. No. 5.4e-56;
Matches 255; Conservative 23; Mismatches 17; Indels 0; Gaps 0;

QY 2 TMNDFDYLLKLGKGTGKGVILVREKASGKYAMKILKKEVIAKDEVAHTLTESRLVKNT 61
DB 148 TMNDFDYLLKLGKGTGKGVILVREKATGRYYAMKILKKEVIAKDEVAHTLTESRLVQNT 207

QY 62 RHPFLTSLKYSFQTKDRLCFVMEYVNGGELFFHLSRERVFSEDRTRFYGAIVSALDYHL 121
DB 208 RHPFLTALKYAFQTHDRLCFVMEYANGGELFFHLSRERVFTEERARFYGAIVSALEYHL 267

QY 122 SGKIVYRDLKLENMLDKDGHKITDPGLCKEGITDAATMKTFCGTPEYLAPEVLENDY 181
DB 268 SRDVVYRDIKLENMLDKDGHKITDPGLCKEGISDGMKTFCGTPEYLAPEVLENDY 327

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**Query Match**

**Best Local Similarity** 88.2%; Score 1378.5; DB 1; Length 480;  
**Matches** 258; Conservative 20; Mismatches 17; Indels 1; Gaps 1;

**Query** 2 TMNDFYKLLGKGTFGKVILVREKASGGKYAMKILKKVEIIIAKDEVAHTLTESRVLKNT 61  
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :  
**Dbb** 146 TMEFEYVKLLGKTFPGKVIIVKEKATAAYYAMKILAKVEIIVAKDEVAHTLTENRVLQNS 205  
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :

**Query** 62 RHPFLTSIKYSFQTKDLRCFWMEYNGGELFFHLRSRRVSSEDRTPRYGAIEVSALDYH 121  
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :  
**Dbb** 206 RHPSLTALKYSFQTHRLCLCFWMEYANGGELFFHLRSRRVSSEDRARFYGAIEVSALDYH 265  
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :

**Query** 122 SGK-IVVRDLEKLNLMDKOGHKITDPGLCKEGITDAATMKTFCGPPEYLAPLEVLDND 180  
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :  
**Dbb** 266 SEKEVVTRDLKENLMIDKOGHKITDPGLCKEGIKOGATMKTCGPTPEYLAPLEVLEDND 325  
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :

**Query** 181 YGRAVDWMGLGVVMYCGRLPFPYNODHEKLFELLIMEDIKFPRTLUSSDAKSLLSGLLI 240  
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :  
**Dbb** 328 GRAVDWMGLGVVMYCGRLPFPYNODHERLFPFNQDHRLFELLIMEEIRFPRTLSPKAISLAGLLXK 387  
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :

**Query** 242 DPNKRLLGGGPDPAKETMRHSFFSGVNWDVYDKLVPPPKPQVTSETDTFRDEE 296  
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :  
**Dbb** 388 DPQRLLGGGSDPAKEVMHRFFLSINQDVQKQLLPPFKPQVTSEVDTRYFDDE 442  
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :

**RESULT 9**

S62117

N;Alternate names: protein kinase B alpha; RAC-PK-alpha; serine/threonine-specific protease C;Species: Bos primigenius taurus (cattle)  
C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text\_change 16-Aug-2004  
A;Accession: S62117; S24423; S17999; S15714; S36388  
R;Coffer, P.J.; Woodgett, J.R.  
submitted to the EMBL Data Library, December 1991  
A;Reference number: S62117  
A;Accession: S62117  
A;Molecule type: mRNA  
A;Residues: 1-480 <COF>  
A;Cross-references: UNIPROT:Q01314; UNIPARC:UPI000012B042; EMBL:X61036; NID:g630; PIDN:C17999  
A;Note: This is a revision to the sequence from reference S17999  
R;Coffer, P.J.; Woodgett, J.R.  
Eur. J. Biochem. 205, 1217, 1992  
A;Reference number: S24423; MUID:92249329; PMID:1533586  
A;Contents: erratum  
A;Accession: S24423  
A>Status: nucleic acid sequence not shown  
A;Molecule type: mRNA  
A;Residues: 70-78, 'N', 80-145 <COW>  
A;Cross-references: UNIPARC:UPI00001725AD; EMBL:X61036  
A;Note: This is a revision to the sequence from reference S17999  
R;Coffer, P.J.; Woodgett, J.R.  
Eur. J. Biochem. 201, 475-481, 1991  
A>Title: Molecular cloning and characterisation of a novel putative protein-serine kinase  
A;Reference number: S17999; MUID:92037600; PMID:1718748  
A;Accession: S17999  
A;Molecule type: mRNA  
A;Residues: 1-70, 'TPSSAACGPRSSARSSTWRPRSCGVDRHRHDGGRRAQAAGGGDDGPLVGTLRELGGRGDGVGAGOA'  
A;Cross-references: UNIPARC:UPI0001725AB; EMBL:X61036  
A;Note: This sequence has been revised in references S62117 and S24423  
C;Function:  
A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threoninophosphate by signal transduction pathways regulating various processes  
C;Superfamily: RAC serine/threonine-protein kinase; pleckstrin repeat homology; protein kinase family; ATP; autophosphorylation; phosphoprotein; phosphotransferase; proto-oncogene F;4-106/Domain: pleckstrin repeat homology <PLK>  
F;148-408/Domain: protein kinase homology <KIN>  
F;156-164/Region: protein kinase ATP-binding motif  
F;179/Active site: Lys phosphate predicted  
F;308/Binding site: Phosphate (Thr) (covalent) (by phosphorylation)  
F;473/Binding site: Phosphate (Ser) (covalent) (by autophosphorylation)



F;199-207/Region: protein kinase ATP-binding motif  
F;222/Active site: Lys #status predicted  
F;350/Binding site: phosphate (Thr) (covalent) #status predicted  
F;517/Binding site: phosphate (Ser) (covalent) (by autophosphorylation) #status predicted

Query Match 70.2%; Score 1098; DB 1; Length 541;  
Best Local Similarity 68.5%; Pred. No. 8e-43;  
Matches 202; Conservative 39; Mismatches 54; Indels 0; Gaps 0;

Qy 2 TMNDFYLLKLGKGTGFKVILVREKASGKYAMKILKKEVIIAKDEVAHFLTESRVLKNT 61  
Db 189 TMEDFDFLKLKLGKGTGFKVILCKEKTQKLYAIKILKKOVIIAREEVAHFLTENVLQRC 248  
Qy 62 RHPFLTSKYSPQTKORLCFVMEYVNGELFFHLSRERVSEDRTRFYGAIEIVSALDYHL 121  
Db 249 KHPELTSLKYSFQHQYLCFVMOFANGELFTVHRKCGTSEPRARFYGAIEIVLALGYLH 308  
Qy 122 SGKIVYRDLKLENLMDKDGHIKTDFGLCKEGITDAATMKTCGTPGYLAPEVLSDNDY 181  
Db 309 RCDIVYRDMKLENLLDKDGHIKIADFGLCCKEISFGDKTSTFCGTPGYLAPEVLDDHDY 368  
Qy 182 GRAVDWGLGVVYEMMCGRLPFYVNDQHEKLFELILMEDIKFPRITSSDAKSLSGLLIK 241  
Db 369 GRCVDWGLGVVYEMMCGRLPFVSKDHNLKLFELIMAGDLRFPSKLSQEARLTLLGLVYK 428  
Qy 242 DPNKRLGGGDDDAKEIMRHSSFFSGVNNQDVYDKLVPPFPQVTSSETDTRYFDEE 296  
Db 429 DPTQLRGSGPEDALEICRADFFRTVDWEATYKEIEPPYKPNVQSETDTSYFONE 483

RESULT 14  
T21523  
protein kinase (EC 2.7.1.37) akt-2 long splice form [similarity] - Caenorhabditis elegans  
N;Alternate names: PKB; protein kinase B  
C;Species: Caenorhabditis elegans  
C;Date: 31-Mar-2001 #sequence-revision 31-Mar-2001 #text\_change 16-Aug-2004  
C;Accession: T21523; T23878  
R;McMurray, A.  
submitted to the EMBL Data Library, September 1998  
A;Reference number: Z19434  
A;Accession: T21523  
A;Status: translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-528 <W1>  
A;Cross-references: UNIPROT:Q9XTG7; UNIPARC:UPI0000076045; EMBL:AL031621; PIDN:CAA20936.  
A;Experimental source: clone F28H6  
R;McMurray, A.  
submitted to the EMBL Data Library, March 1997  
A;Reference number: Z19812  
A;Accession: T23878  
A;Status: translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-528 <W12>  
A;Cross-references: UNIPARC:UPI0000076045; EMBL:Z92837; PIDN:CAB07403.1; GSPDB:GN000028;  
A;Experimental source: clone R03E1  
C;Genetics:  
A;Gene: akt-2; CESP:F28H6.1  
A;Map position: X  
A;Introns: 32/2; 68/3; 135/3; 175/3; 241/3; 285/2; 305/3; 348/3; 459/3  
C;Function:  
A;Description: catalyzes the formation of peptidyl-serine-phosphate or peptidyl-threonine-phosphate  
A;Pathway: signal transduction pathways regulating metabolism, development, and longevity  
A;Superfamily: RAC serine/threonine-protein kinase; pleckstrin repeat homology; protein  
C;Keywords: alternative splicing; ATP; autophosphorylation; phosphoprotein; phosphotransferase  
F;11-113/Domain: pleckstrin repeat homology <PLK>  
F;178-437/Domain: protein kinase homology <KIN>  
F;186-194/Region: protein kinase ATP-binding motif  
F;209/Active site: Lys #status predicted  
F;337/Binding site: phosphate (Thr) (covalent) #status predicted  
F;505/Binding site: phosphate (Ser) (covalent) (by autophosphorylation) #status predicted

Query Match 66.0%; Score 1032; DB 1; Length 528;  
Best Local Similarity 65.8%; Pred. No. 7.1e-40;

Db 416 VPAKRLGAGPDDAREVSRAEFFKQVDWEATLRKEVEPPFKENNANSETDTSEFFD 468

Search completed: February 13, 2006, 06:42:03  
Job time : 74 secs

GenCore version 5.1.7  
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OM nucleic - nucleic search, using sw model

Run on: February 15, 2006, 05:32:58 ; Search time 197 Seconds  
(without alignments)  
8824.646 Million cell updates/sec

Title: US-10-601-311-2  
Perfect score: 978  
Sequence: 1 tctacaaccatcataaaag.....atggtatgactgatgcacg 978

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents NA.\*  
1: /cgn2\_6/prodata/1/ina/1 COMB.seq.\*  
2: /cgn2\_6/prodata/1/ina/5 COMB.seq.\*  
3: /cgn2\_6/prodata/1/ina/6A COMB.seq.\*  
4: /cgn2\_6/prodata/1/ina/6B COMB.seq.\*  
5: /cgn2\_6/prodata/1/ina/H COMB.seq.\*  
6: /cgn2\_6/prodata/1/ina/PCTUS COMB.seq.\*  
7: /cgn2\_6/prodata/1/ina/PP COMB.seq.\*  
8: /cgn2\_6/prodata/1/ina/RE COMB.seq.\*  
9: /cgn2\_6/prodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	978	100.0	1547	3	US-09-851-670-1
2	949.8	97.1	1570	3	US-09-526-043-1
3	689	70.4	2410	3	US-09-771-161A-66
4	525	53.7	2826	3	US-09-590-740-5
5	515.8	52.7	1599	3	US-09-256-465-1
6	515.8	52.7	1599	3	US-09-167-322-3
7	515.8	52.7	1599	3	US-09-023-655-1004
8	510.6	52.2	2181	3	US-09-417-197-70
9	510.6	52.2	2184	3	US-09-417-197-138
10	510.6	52.2	2610	2	US-09-212-771-1
11	510.6	52.2	2610	3	US-09-091-058-1
12	510.6	52.2	2610	3	US-09-023-655-1206
13	510.6	52.2	2610	3	US-09-590-740-1
14	493	50.4	1254	3	US-09-590-740-3
15	383.8	39.2	387	3	US-09-474-922A-2
16	266.4	27.2	2239	3	US-09-949-016-1676
17	261.2	26.7	3255	3	US-09-016-434-1471
18	261.2	26.7	6102	3	US-09-949-016-2007
19	260.4	26.6	2370	3	US-09-031-295-1
20	260.4	26.6	2370	3	US-10-000-039-1
21	260.2	26.6	265	3	US-09-513-999C-2948
22	258.8	26.5	1338	3	US-10-067-977-1
23	257.6	26.3	2599	9	5266464-1
24	257.2	26.3	2311	2	US-08-712-709-6

25	257.2	26.3	2311	3	US-09-111-444-6	Sequence 6, Appli
26	257.2	26.3	2311	3	US-09-541-228-6	Sequence 6, Appli
27	257.2	26.3	2311	3	US-09-016-434-772	Sequence 772, App
28	255.8	26.2	2396	3	US-09-949-016-1735	Sequence 1735, Ap
29	246.4	25.2	3321	3	US-09-023-655-1361	Sequence 1361, Ap
30	240.4	24.6	2245	3	US-09-225-749-24	Sequence 24, Appli
31	239.4	24.5	2274	3	US-09-772-647-3	Sequence 3, Appli
32	239.4	24.5	2274	3	US-10-228-931-3	Sequence 3, Appli
33	238.6	24.0	532	3	US-09-270-767-14090	Sequence 14090, A
34	235.2	24.0	3456	3	US-09-487-558B-265	Sequence 265, App
35	233.2	23.8	2556	3	US-09-817-310-1	Sequence 1, Appli
36	233.2	23.8	2556	3	US-10-355-724A-1	Sequence 1, Appli
37	232	23.7	2244	3	US-09-094-714A-48	Sequence 48, Appli
38	229.8	23.5	1413	3	US-09-248-796A-4379	Sequence 4379, Ap
39	225.4	23.0	2127	3	US-09-270-767-13509	Sequence 13509, A
40	222.4	22.7	2346	3	US-09-762-258-3	Sequence 3, Appli
41	219.8	22.5	2751	3	US-09-417-197-72	Sequence 72, Appli
42	214.8	22.0	2324	3	US-09-190-976B-6	Sequence 6, Appli
43	213.6	21.8	2705	3	US-09-949-016-839	Sequence 839, App
44	213.6	21.8	2715	3	US-09-949-016-1959	Sequence 1959, Ap
45	212	21.7	2754	3	US-09-429-322-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1  
US-09-851-670-1  
; Sequence, Application US/09851670  
; Patent No. 6809194  
; GENERAL INFORMATION:  
; APPLICANT: Reinhard, Christoph  
; APPLICANT: Jefferson, Anne B.  
; TITLE OF INVENTION: AKT3 INHIBITORS  
; FILE REFERENCE: PP-01699.002/200130.520  
; CURRENT APPLICATION NUMBER: US/09/851,670  
; CURRENT FILING DATE: 2001-05-08  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 1547  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-851-670-1

Query Match 100.0%; Score 978; DB 3; Length 1547;  
Best Local Similarity 100.0%; Pred. No. 1.1e-267;  
Matches 978; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	TCTACAACCCATCATATAAAGAACATGAATGATTTTGACTATTTGAACTACTAGGT	60
DB	416	TCTACAACCCATCATATAAAGAACATGAATGATTTTGACTATTTGAACTACTAGGT	475
QY	61	AAAGCAGCTTTGGGAAAGTATTTTGGTTCAGAGAGGCAAGTGGAAAACTATGCT	120
DB	476	AAAGCAGCTTTGGGAAAGTATTTTGGTTCAGAGAGGCAAGTGGAAAACTATGCT	535
QY	121	ATGAAGATTCTCAAGAAAGAGTCAATTATTGCAAGAGGATGAAGTGGCACACACTCTAACT	180
DB	536	ATGAAGATTCTCAAGAAAGAGTCAATTATTGCAAGAGGATGAAGTGGCACACACTCTAACT	595
QY	181	GAAAGCAGAGTATTAAGAAACACTAGACATCCCTTTTAAACATCCCTTTGAAATATTCCTTC	240
DB	596	GAAAGCAGAGTATTAAGAAACACTAGACATCCCTTTTAAACATCCCTTTGAAATATTCCTTC	655
QY	241	CAGACAAAGACCGTTTGTGTTTGTGATGGAATATGTTAAATGGGGCGGCGGCTGTTTTC	300
DB	656	CAGACAAAGACCGTTTGTGTTTGTGATGGAATATGTTAAATGGGGCGGCGGCTGTTTTC	715
QY	301	CATTTGTGAGAGAGCGGCTGTTTCTCTGAGAGCCGACACACGTTTCTATGTCGAGAAAT	360
DB	716	CATTTGTGAGAGAGCGGCTGTTTCTCTGAGAGCCGACACACGTTTCTATGTCGAGAAAT	775

Qy 361 GTCTCTGCTTGGACTATCTACATTCGGAAGAAGATTGTGTACCGTGATCTCAAGTTGGAG 420  
Db |||||  
Qy 776 GTCTCTGCTTGGACTATCTACATTCGGAAGAAGATTGTGTACCGTGATCTCAAGTTGGAG 835  
Db |||||  
Qy 421 AATCTAATGCTGGCAAGATGGCCACATATAAATTTACAGATTTTGACATTTGCAAGAA 480  
Db |||||  
Qy 836 AATCTAATGCTGGCAAGATGGCCACATATAAATTTACAGATTTTGACATTTGCAAGAA 895  
Db |||||  
Qy 481 GGGATCACAGATGCAGCACCACCATGAAGACATTTCTGTGCGACTCTCAGAAATATCTGGCACCA 540  
Db |||||  
Qy 896 GGGATCACAGATGCAGCACCACCATGAAGACATTTCTGTGCGACTCTCAGAAATATCTGGCACCA 955  
Db |||||  
Qy 541 GAGGTGTTAGAATAATGACTATGCGCGAGCAGTAGACTGGTGGGCGCTAGGGGTTGTC 600  
Db |||||  
Qy 956 GAGGTGTTAGAATAATGACTATGCGCGAGCAGTAGACTGGTGGGCGCTAGGGGTTGTC 1015  
Db |||||  
Qy 601 ATGTATGAATGATGTGGGAGGTTACCTTTCTCAACAGGACCATGAGAACTTTTT 660  
Db |||||  
Qy 1016 ATGTATGAATGATGTGGGAGGTTACCTTTCTCAACAGGACCATGAGAACTTTTT 1075  
Db |||||  
Qy 661 GAATTAATATTAATGGAAGACATTTAAATTTCTCGAACACTCTCTTCAGATGCAAAATCA 720  
Db |||||  
Qy 1076 GAATTAATATTAATGGAAGACATTTAAATTTCTCGAACACTCTCTTCAGATGCAAAATCA 1135  
Db |||||  
Qy 721 TTGCTTTTCAGGCTCTTTGATAAAGGATCCAAATAAAGCGCTTGGTGAGGACCAAGATGAT 780  
Db |||||  
Qy 1136 TTGCTTTTCAGGCTCTTTGATAAAGGATCCAAATAAAGCGCTTGGTGAGGACCAAGATGAT 1195  
Db |||||  
Qy 781 GCAAAAGAAATTTAGACACAGTTTCTCTCGAGTAACTGGCAAGATGATATGAT 840  
Db |||||  
Qy 1196 GCAAAAGAAATTTAGACACAGTTTCTCTCGAGTAACTGGCAAGATGATATGAT 1255  
Db |||||  
Qy 841 AAAAGCTTGTACCTCTTTTAAACCTCAAGTAACATCTGAGACAGATCTAGATATTTT 900  
Db |||||  
Qy 1256 AAAAGCTTGTACCTCTTTTAAACCTCAAGTAACATCTGAGACAGATCTAGATATTTT 1315  
Db |||||  
Qy 901 GATGAAGAATTTACAGCTCAGACTATTACAATAACACCACTGAAAAATATGATGAGGAT 960  
Db |||||  
Qy 1316 GATGAAGAATTTACAGCTCAGACTATTACAATAACACCACTGAAAAATATGATGAGGAT 1375  
Db |||||  
Qy 961 GGTATGACTGCATGGAC 978  
Db |||||  
Qy 1376 GGTATGACTGCATGGAC 1393  
Db |||||

RESULT 2

US-09-526-043-1  
; Sequence 1, Application US/09526043  
; Patent No. 6881555  
; GENERAL INFORMATION:  
; APPLICANT: Guo, Kun  
; APPLICANT: Pagnoni, Marco  
; APPLICANT: Clark, Kenneth  
; APPLICANT: Ivashchenko, Yuri  
; TITLE OF INVENTION: AKT NUCLEIC ACIDS, POLYPEPTIDES, AND USES THEREOF  
; FILE REFERENCE: A3278A-US  
; CURRENT APPLICATION NUMBER: US/09/526.043  
; CURRENT FILING DATE: 2000-03-14  
; EARLIER APPLICATION NUMBER: 60/125,108  
; EARLIER FILING DATE: 1999-03-19  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 1570  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (126)..(1523)  
US-09-526-043-1

Query Match 97.1%; Score 949.8; DB 3; Length 1570;  
Best Local Similarity 99.8%; Pred. No. 1.2e-259;

Matches 951; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Qy 1 TCTACAAACCCATCATAAAGAAAGACAAATGAATGATTTTGACTATTTGAAACTACTAGGT 60  
Db |||||  
Qy 531 TCTACAAACCCATCATAAAGAAAGACAAATGAATGATTTTGACTATTTGAAACTACTAGGT 590  
Db |||||  
Qy 61 AAAGGCACATTTTGGGAAAGTTATTTTGGTTCGAGAGAAGGCAAGTGGAAATATCTATGCT 120  
Db |||||  
Qy 591 AAAGGCACATTTTGGGAAAGTTATTTTGGTTCGAGAGAAGGCAAGTGGAAATATCTATGCT 650  
Db |||||  
Qy 121 ATGAAGATTTCTGAAGAAAGAAAGTCATTTATTTGCAAAAGGATGAAGTGGCACACACTCTAACT 180  
Db |||||  
Qy 651 ATGAAGATTTCTGAAGAAAGAAAGTCATTTATTTGCAAAAGGATGAAGTGGCACACACTCTAACT 710  
Db |||||  
Qy 181 GAAAGCAGAGTATTTAAAGAACACTAGACATCCCTTTTTTAACATCCTTTGAAATATTTCTTTC 240  
Db |||||  
Qy 711 GAAAGCAGAGTATTTAAAGAACACTAGACATCCCTTTTTTAACATCCTTTGAAATATTTCTTTC 770  
Db |||||  
Qy 241 CAGACAAAAGACCGTTTGTCTTTTGTGATCGAAATATGTTAATGGGGCGGAGCTGTTTTTC 300  
Db |||||  
Qy 771 CAGACAAAAGACCGTTTGTCTTTTGTGATGGAATATGTTAATGGGGCGGAGCTGTTTTTC 830  
Db |||||  
Qy 301 CATTTGTCGAGAGAGCGGGTGTCTCTGAGGACCGGCACACGTTTCTATGTTGCGAATAATT 360  
Db |||||  
Qy 831 CATTTGTCGAGAGAGCGGGTGTCTCTGAGGACCGGCACACGTTTCTATGTTGCGAATAATT 890  
Db |||||  
Qy 361 GTCTCTGCTTGGACTATCTACATTCGGAAGAAGATTGTGTACCGTGATCTCAAGTTGGAG 420  
Db |||||  
Qy 891 GTCTCTGCTTGGACTATCTACATTCGGAAGAAGATTGTGTACCGTGATCTCAAGTTGGAG 950  
Db |||||  
Qy 421 AATCTAATGCTGGCAAGATGGCCACATATAAATTTACAGATTTTGACATTTTGCAGAA 480  
Db |||||  
Qy 951 AATCTAATGCTGGCAAGATGGCCACATATAAATTTACAGATTTTGACATTTTGCAGAA 1010  
Db |||||  
Qy 481 GGGATCACAGATGCAGCACCACCATGAAGACATTTCTGTGCGACTCTCAGAAATATCTGGCACCA 540  
Db |||||  
Qy 1011 GGGATCACAGATGCAGCACCACCATGAAGACATTTCTGTGCGACTCTCAGAAATATCTGGCACCA 1070  
Db |||||  
Qy 541 GAGGTGTTAGAAGATTAATGACTATGCGCGAGCAGTAGACTGGTGGGCGCTAGGGGTTGTC 600  
Db |||||  
Qy 1071 GAGGTGTTAGAAGATTAATGACTATGCGCGAGCAGTAGACTGGTGGGCGCTAGGGGTTGTC 1130  
Db |||||  
Qy 601 ATGTATGAATGATGTGTGGAGGTTTACCTTTCTACAACAGGACCACTGAGAACTTTTT 660  
Db |||||  
Qy 1131 ATGTATGAATGATGTGTGGAGGTTTACCTTTCTACAACAGGACCACTGAGAACTTTTT 1190  
Db |||||  
Qy 661 GAATTAATATTAATGGAAGACATTTAAATTTCTCGAACACTCTCTTCAGATGCAAAATCA 720  
Db |||||  
Qy 1191 GAATTAATATTAATGGAAGACATTTAAATTTCTCGAACACTCTCTTCAGATGCAAAATCA 1250  
Db |||||  
Qy 721 TTGCTTTTCAGGGCTCTTTGATAAAGGATCCAAATAAAGCGCTTGGTGAGGACCAAGATGAT 780  
Db |||||  
Qy 1251 TTGCTTTTCAGGGCTCTTTGATAAAGGATCCAAATAAAGCGCTTGGTGAGGACCAAGATGAT 1310  
Db |||||  
Qy 781 GCAAAAGAAATTTAGACACAGTTTCTCTCTCGAGTAAACTGGCAAGATGTATATGAT 840  
Db |||||  
Qy 1311 GCAAAAGAAATTTAGACACAGTTTCTCTCTCGAGTAAACTGGCAAGATGTATATGAT 1370  
Db |||||  
Qy 841 AAAAGCTTGTACCTCTTTTAAACCTCAAGTAACATCTGAGACAGATCTAGATATTTT 900  
Db |||||  
Qy 1371 AAAAGCTTGTACCTCTTTTAAACCTCAAGTAACATCTGAGACAGATCTAGATATTTT 1430  
Db |||||  
Qy 901 GATGAAGAATTTACAGCTCAGACTATTACAATAACACCACTGAAAAATATGA 953  
Db |||||  
Qy 1431 GATGAAGAATTTACAGCTCAGACTATTACAATAACACCACTGAAAAATATGA 1483  
Db |||||

RESULT 3

US-09-771-161A-66  
; Sequence 66, Application US/09771161A  
; Patent No. 6936450  
; GENERAL INFORMATION:  
; APPLICANT: LEVINE, et al.



; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES  
; FILE REFERENCE: 802620-2005.1  
; CURRENT APPLICATION NUMBER: US/09/771,161A  
; CURRENT FILING DATE: 2001-01-26  
; PRIOR APPLICATION NUMBER: 09/724,676  
; PRIOR FILING DATE: 2000-11-28  
; PRIOR APPLICATION NUMBER: 136776  
; PRIOR FILING DATE: 2000-06-15  
; PRIOR APPLICATION NUMBER: 135619  
; PRIOR FILING DATE: 2000-04-12  
; NUMBER OF SEQ ID NOS: 273  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 66  
; LENGTH: 2410  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-771-161A-66

Query Match 70.4%; Score 689; DB 3; Length 2410;  
Best Local Similarity 100.0%; Pred. No. 1.8e-185; Indels 0; Gaps 0;  
Matches 689; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 290 AGCTGTTTTCATTTGTCGAGAGCGGGTGTCTCTGAGGACCGCACACCGTTTCTATG 349  
DB 312 AGCTGTTTTCATTTGTCGAGAGCGGGTGTCTCTGAGGACCGCACACCGTTTCTATG 371  
QY 350 GTGCAAAATTTCTCTGCTTGGACTATCTACATTCGCGAAAGATTGTGTACCGTGATC 409  
DB 372 GTGCAAAATTTCTCTGCTTGGACTATCTACATTCGCGAAAGATTGTGTACCGTGATC 431  
QY 410 TCAAGTTGGAGATCTAATGCTGGGCAAGATGGCCACATAAAATTCAGATTTTGGAC 469  
DB 432 TCAAGTTGGAGATCTAATGCTGGGCAAGATGGCCACATAAAATTCAGATTTTGGAC 491  
QY 470 TTTGCAAAAGAGGATCACAGATGAGCCACCATGAAGACATTTCTGTGGCACTCCAGAT 529  
DB 492 TTTGCAAAAGAGGATCACAGATGAGCCACCATGAAGACATTTCTGTGGCACTCCAGAT 551  
QY 530 ATCTGGCACAGAGGTGTTAGAGATAATGACTATGGCCGAGCAGTAGACTGTGGGGCC 589  
DB 552 ATCTGGCACAGAGGTGTTAGAGATAATGACTATGGCCGAGCAGTAGACTGTGGGGCC 611  
QY 590 TAGGGGTGTCTATGAAATGATGTGGGAGGTACCTTTCTACAAACAGGACCATG 649  
DB 612 TAGGGGTGTCTATGAAATGATGTGGGAGGTACCTTTCTACAAACAGGACCATG 671  
QY 650 AGAAACTTTTTCGAAATTAATTAATGAAGACATTAATAATTTCTCGAACACTCTCTTCAG 709  
DB 672 AGAAACTTTTTCGAAATTAATTAATGAAGACATTAATAATTTCTCGAACACTCTCTTCAG 731  
QY 710 ATGCAAAATTCATTTGCTTTTCAGGGCTCTTGATAAAGGATCCAAATAAAGCCCTTGGTGGAG 769  
DB 732 ATGCAAAATTCATTTGCTTTTCAGGGCTCTTGATAAAGGATCCAAATAAAGCCCTTGGTGGAG 791  
QY 770 GACCAAGATGATGCAAAAGAAATTAAGACACAGATTTCTTCTGTGGAGTAAACTGGCAAG 829  
DB 792 GACCAAGATGATGCAAAAGAAATTAAGACACAGATTTCTTCTGTGGAGTAAACTGGCAAG 851  
QY 830 ATGTATATGATAAAGCTTTGACTCTCTTTTAAACCTCAAGTAAACATCTGAGACAGATA 889  
DB 852 ATGTATATGATAAAGCTTTGACTCTCTTTTAAACCTCAAGTAAACATCTGAGACAGATA 911  
QY 890 CTAGATATTTTGTATGAAGATTTACAGCTCAGACTATTACAAATAACACCACTGAAAT 949  
DB 912 CTAGATATTTTGTATGAAGATTTTACAGCTCAGACTATTACAAATAACACCACTGAAAT 971  
QY 950 ATGATGAGGATGGTATGGACTGATGGAC 978  
DB 972 ATGATGAGGATGGTATGGACTGATGGAC 1000

RESULT 4  
US-09-590-740-5

; Sequence 5, Application US/09590740  
; Patent No. 6889807  
; GENERAL INFORMATION:  
; APPLICANT: Kenneth Walsh  
; TITLE OF INVENTION: HMG CoA Reductase Inhibitors for  
; TITLE OF INVENTION: Promoting Angiogenesis  
; FILE REFERENCE: 49,784 (1417)  
; CURRENT APPLICATION NUMBER: US/09/590,740  
; CURRENT FILING DATE: 2000-06-08  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 5  
; LENGTH: 2626  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-09-590-740-5

Query Match 53.7%; Score 525; DB 3; Length 2626;  
Best Local Similarity 73.4%; Pred. No. 7.5e-139; Indels 3; Gaps 1;  
Matches 685; Conservative 0; Mismatches 245; Indels 3; Gaps 1;  
QY 24 GACAAATGAATGATTTTGACTATTTGAACTACTAGTAAAGGCACCTTTTGGGAAAGTAT 83  
DB 718 GACCAATGAACGATTTTGACTACTGAACTACTTGGCAAGGCGACCTTTGGGAAAGTAT 777  
QY 84 TTTGGTTTCGAGAGAGGCAAGTGGAAATATCTATGCTATGAAGATTTCTGAAGAAAGAGT 143  
DB 778 TCTGCTGAAAGAGAGAGGCCACAGCGCGTACTATGCCATGAAGATCCTCAAGAGAGGCT 837  
QY 144 CATTAATGCAAGGATGAAGTGGCACACACTCTAACTGAAACAGAGATTTAAAGAACAC 203  
DB 838 CATCTGTCGCAAGGATGAGTTGCCCCACACGCTTACTGAGAACCGTGTCTCGAGAACTC 897  
QY 204 TAGACATCCCTTTTAAACATCCTTGAATATATCTTTCAGACAAAGACCGTTTGTGTTT 263  
DB 898 TAGGATATCCCTTCTTACGGCCCTCAAGTACTCATTCAGACCCAGCCGCTCTGCTT 957  
QY 264 TGTGATGGAATATGTTAATGGGGCGAGCTGTTTTTCCATTTGTGAGAGAGCGGTGTT 323  
DB 958 TGTGATGAGTATGCCAACGGGGCGAGCTCTTCTTCCACCTGTCTCGAGAGCGCGTGT 1017  
QY 324 CTCTGAGACCGCACACGTTTCTATGTTGTCAGAAATTTGTCTCTGCTTGGACTATCTACA 383  
DB 1018 CTCCGAGGACCGGGCCGCTTCTATGTTGTCGAGATTTGTCTGCTGCTGACTTGTGA 1077  
QY 384 TTCCGGGAAAGA---TTGTGTACCGTGATCTCAAGTTTGGAGATCTAACTCTCGACAAAGA 440  
DB 1078 CTCCGAGAGAAACGCTGTGTACCGGACCTGAGCTGAGAAACCTCATGCTCGACAAAGA 1137  
QY 441 TGGCCACATAAAATTTACAGATTTTGGACTTTTGCAGAAAGGAGTACAGATGCAAGCCAC 500  
DB 1138 CGGGCACATCAAGATAACGACTTCGGGCTGTGCAAGGAGGGGATCAAGGATGGTCCAC 1197  
QY 501 CATGAAGACATTTCTGTGGCACTCCAGAAATATCTGSCACAGAGGTGTTAGAAGATAATGA 560  
DB 1198 TATGAAGACATTTCTCGGAAACGCGGAGTACCTGGCCCTGTGAGGTGCTCGAGGACAA 1257  
QY 561 CTATCGCCGAGCAGTAGACTGTGGGGCTTAGGGGTGTGTCATGATGAATGATGTGTCG 620  
DB 1258 CTACGGCCGTGAGTGGACTGTGGGGCTGTGGCGGTGTGTCATGATGATGATGTGTGG 1317  
QY 621 GAGGTTTACCTTTCTACAAACAGGACCATGAGAAATTTTTTGAATTAATTAATGAAGA 680  
DB 1318 CGCCCTGCTTCTACAAACAGGACCATGAGAAAGCTGTTCGAGCTGATCCTCATGGAGA 1377  
QY 681 CATTAATTTCTCGAAACACTCTCTTTCAGATGCAAAATCATTTGCTTTAGGGCTCTTGT 740  
DB 1378 GATCGCTTCCGCGCACACTCGGCCCTGAGGCCAAGTCCCTGCTCTCGGGCTGTCTCAA 1437  
QY 741 AAGGATCCAAATAAACCGCTTGTGGAGGACAGATGATGCAAAAGAAATTTATGAGACA 800  
DB 1438 GAAGGACCTTACACAGAGGCTCGTGGGGGCTCTGAGGATGCAAGGAGATCATGCAGCA 1497

Qy 801 CAGTTTCTTCTCTGAGTAATACTGGCAAGATGTATATGATAAAAGCTTGTACCTCTTT 860  
Db 1498 CCGGTTCTTTGCCAACATCGTGTGGCAGGATGTGTATGAGAAGAGCTGAGCCACCTTT 1557  
Qy 861 TAAACCTCAAGTAATCTGAGACAGATACAGATATTTTGTATGAAGATTTAGAGCTCA 920  
Db 1558 CAAGCCCGAGGTACCTCTGAGACTGACACAGGTATTTTCATGAGGAGTTTACAGCTCA 1617  
Qy 921 GACTATTACATAACACACCTGAAAATATGA 953  
Db 1618 GATGATCACCATACCGCGCCTGATCAAGATGA 1650

RESULT 5  
US-09-256-465-1  
; Sequence 1, Application US/09256465  
; Patent No. 6043090  
; GENERAL INFORMATION:  
; APPLICANT: Brett P. Monia  
; APPLICANT: Lex M. Cowert  
; TITLE OF INVENTION: ANTISENSE MODULATION OF AKT-2 EXPRESSION  
; FILE REFERENCE: RGS-0035  
; CURRENT APPLICATION NUMBER: US/09/256,465  
; CURRENT FILING DATE: 1999-02-23  
; NUMBER OF SEQ ID NOS: 47  
; SEQ ID NO 1  
; LENGTH: 1599  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (88)..(1533)  
US-09-256-465-1

Query Match 52.7%; Score 515.8; DB 3; Length 1599;  
Best Local Similarity 72.0%; Pred. No. 2.5e-136;  
Matches 673; Conservative 0; Mismatches 262; Indels 0; Gaps 0;

Qy 19 AGAAGACATGAATGATTTTGACTATTTGAACTACTAGTAAGGACCTTTGGGAAA 78  
Db 523 AAAGTGACCATGAATGATCTCGACTATCTCAAACTCTTGGCAAGGAAACCTTTGGCAAA 582  
Qy 79 GTTATTTTGGTTCGAGAGAGGCAAGTGGAAATACTATGTAAGAGATCTCAAGAAA 138  
Db 583 GTCATCTGTCGGGAGAGGCCACTGGCCGCTACTACGCCATGAAGATCTCGAAG 642  
Qy 139 GAAGTCATATTGCAAGAGATGAAGTGGCACACACTCTTAAGTGAAGCAGAGATTAAAG 198  
Db 643 GAAGTCATATTGCAAGAGATGAAGTGGCACACAGTCAAGAGAGCCGGTCTCCAG 702  
Qy 199 AACACTAGACATCCCTTTTAAACATCTTGAATATTTCTTCCAGACAAAGACCGTTTG 258  
Db 703 AACACCAAGGACCGGTTTCTCACTGCGCTGAAGTATGCTTTCCAGACCCACACCGCTG 762  
Qy 259 TGTTTTGTGGAATATGTTAAATGGGGCGAGCTGTTTTTCCATTTGTGAGAGAGCGG 318  
Db 763 TGTCTTGTGATGGAGTATGCCAAGGGGTGAGCTGTCTTCCACCTGTCCCGGAGCGT 822  
Qy 319 GTGTTCTCTGAGGACCGCACACGTTTCTATGGTGCAGAAATGTCTCTGCTTGGACTAT 378  
Db 823 GTCTTCACAGAGGAGCGGCCGGTTTATGGTGCAGAGATTGCTCGGCTCTTGAGTAC 882  
Qy 379 CTACATCCGGAAGATTTGTCTACGGTGATCTCAAGTTGGAGATCTTAAGTCTGGACAAA 438  
Db 883 TTGCACTCGCGGGACGTTGTTATCCGCGACATCAAGCTGGAAGAACCTCATGCTGGACAAA 942  
Qy 439 GATGGCCACATAAAATTTACAGATTTTGGACTTTTGCAGAGAGGATCACAGATGCAGCC 498  
Db 943 GATGGCCACATCAAGATCACTGACTTTGGCCCTCTGCAAGAGGGCATCAGTACGGGGCC 1002  
Qy 499 ACCATGAAGACATTTCTGTGGCACTCCAGAAATATCTGGCACAGAGGTGTTTGAAGATAAT 558

Db 1003 ACCATGAAAACCTTCTGTGGGACCCCGGAGTACCTGCGGCTGAGGTGCTGGAGACAAT 1062  
Qy 559 GACTATGGCGAGCAGTAGACTGTGTGGGGCTAGGGGTGTGTCATGTATGAAATGATGTGT 618  
Db 1063 GACTATGGCGGGCGCTGGACTGTGTGGGGCTGGGTGTGTCATGTACGAGATGATGTGC 1122  
Qy 619 GGGAGGTTACCTTTCTACAACCCAGGACCATGAGAAACTTTTGTGAATTAATTAATGAA 678  
Db 1123 GGGCGCTGCGCTTCTACAACCCAGGACCATGAGGCGCTCTTCGAGCTCATCTCATGGAA 1182  
Qy 679 GACATTAATTTCTCGAACACTCTCTTCAGATGCAAAATCATTTCTCAGGCTCTTG 738  
Db 1183 GAGATCGCTTCCGCGCAGCTCAGCCCGAGGCGCAAGTCCCTGCTTGTGGGCTGCTT 1242  
Qy 739 ATAAAGGATCCAAATAAACCGCTTGTGGAGGACAGATGATGCAAAAGAAATTAATGAGA 798  
Db 1243 AAGAGGACCCCAAGCAGAGAGCTTGTGGGGGCGCCAGCGATGCCAAGGAGTCAAGAG 1302  
Qy 799 CACAGTTTCTTCTCTGGAGTAAACTGGCAAGATGTATATGATAAAAGCTTTGTACCTCT 858  
Db 1303 CACAGGTTCTTCTCAGCATCAACTGGCAGGACGTTGGTCCAGAAGAAAGCTCCTGCCACC 1362  
Qy 859 TTTAAACCTCAAGTAACATCTGACAGACATAGATATTTTGTGAAGATTTTACAGCT 918  
Db 1363 TTTAAACCTCAGGTACGTCGAGGTCGACACAGGTAAGTCTGATGATGAATTTACCGCC 1422  
Qy 919 CAGACTATTACAATAACACCACTGAAAAATATGA 953  
Db 1423 CAGTCCATCAATCACACCCCTGACCGCTATGA 1457

RESULT 6  
US-09-167-322-3  
; Sequence 3, Application US/09167322  
; Patent No. 636151  
; GENERAL INFORMATION:  
; APPLICANT: Allegheny University of the Health Sciences, Halpern, Michael S. England, James M.  
; TITLE OF INVENTION: CANCER VACCINE  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Seidel, Gonda, Lavorigna & Monaco, P.C.  
; STREET: Suite 1800, Two Penn Center Plaza  
; CITY: Philadelphia  
; STATE: PA  
; COUNTRY: USA  
; ZIP: 19102  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/167,322  
FILING DATE: 07-Oct-1998  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US97/00582  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Monaco, Daniel A.  
REGISTRATION NUMBER: 30,480  
REFERENCE/DOCKET NUMBER: 7933-33 PC  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (215) 568-8383  
TELEFAX: (215) 568-5549  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1599 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 3:  
US-09-167-322-3

Query Match 52.7%; Score 515.8; DB 3; Length 1599;  
Best Local Similarity 72.0%; Pred. No. 2.5e-136;  
Matches 673; Conservative 0; Mismatches 262; Indels 0; Gaps 0;

QY 19 AGAAGACAAATGAATGATTTGACATATTTGAACTACTAGTAAAGGCACTTTTGGGAAA 78  
DB 523 AAAGTGACCATGAATGACTTCGACTATCTCAAACCTCTTGGCAAGGGAACCTTTGGCAAA 582

QY 79 GTTATTTTGGTTCGAGAGAAGCAAGTGGAAATACTATGCTATGAAGATTTCTGAAGAAA 138  
DB 583 GTCATCTCTGGTGGGAGAGGCCACTGGCCGTACTACGCATGAAGATCTGCGAAG 642

QY 139 GAAGTCATTTATGCAAAAGATGAAGTGGCACACACTCTAACTGAAAGCAGAGATTTAAAG 198  
DB 643 GAAGTCATCTTGGCAAGGATGAAGTCGCTCACAGATCACCGAGAGCGGCTCTCCAG 702

QY 199 AACCTAGACATCCCTTTTAACTCTTTTAACTCTTTTAACTCTTTTAACTCTTTTAACTCTTTT 258  
DB 703 AACCTAGACATCCCTTTTAACTCTTTTAACTCTTTTAACTCTTTTAACTCTTTTAACTCTTTT 762

QY 259 TGTATTTGTGATGAATATGTTAAATGGGGCGGAGCTGTTTTCATTTGTCGAGAGAGCGG 318  
DB 763 TGTATTTGTGATGAATATGTTAAATGGGGCGGAGCTGTTTTCATTTGTCGAGAGAGCGG 822

QY 319 GTGTTCTCTGAGGACCGCACACGTTTCTATGTTGTCGAGAAATTTGTCCTGCTTGGACTAT 378  
DB 823 GTCTTCACAGAGAGCGGGCCCGGTTTTATGTTGTCGAGAGATTTGTCCTGCTTGGACTAT 882

QY 379 CTACATTCGGGAAAGATTTGTACGCTGATCTCAAGTTGGAGAAATCTAATGTCGACAAA 438  
DB 883 TTGCACTCGCGGAGCGTGTATACCGGCACATCAAGCTGGAAACCTCATGTCGACAAA 942

QY 439 GATGCCACATAAAATACAGATTTGACATTTGCAAGTTCGAAAGAGGATCACAGATCGCC 498  
DB 943 GATGCCACATCAAGATCACTGACTTTGGCTCTGCAAGAGGGATCAGTACCGGGGCC 1002

QY 499 ACCATGAAGACATCTGTGGCACTCTTCCAGATGCAAAATCATTTGTTTCAAGGGCTCTTG 558  
DB 1003 ACCATGAAGACATCTGTGGCACTCTTCCAGATGCAAAATCATTTGTTTCAAGGGCTCTTG 1062

QY 559 GACTATGGCCGAGCAGTACGCTGTGGGGCCCTAGGGGTTGTCATGTATGAATGATGTG 618  
DB 1063 GACTATGGCCGAGCAGTACGCTGTGGGGCCCTAGGGGTTGTCATGTATGAATGATGTG 1122

QY 619 GGGAGTTACCTTTCTACACAGGACCATGAGAACTTTTGAATTAATTAATGAA 678  
DB 1123 GGGAGTTACCTTTCTACACAGGACCATGAGAACTTTTGAATTAATTAATGAA 1182

QY 679 GACATTAATTTTCTCGAACACTCTTTCAGATGCAAAATCATTTGTTTCAAGGGCTCTTG 738  
DB 1183 GACATTAATTTTCTCGAACACTCTTTCAGATGCAAAATCATTTGTTTCAAGGGCTCTTG 1242

QY 739 ATAAAGGATCCAAATAAAGCCCTTGGTGAGGACACAGATGATGCAAAAGAAATTAAGAA 798  
DB 1243 ATAAAGGATCCAAATAAAGCCCTTGGTGAGGACACAGATGATGCAAAAGAAATTAAGAA 1302

QY 799 CACAGTTTCTCTCGAGTAACTGGCAGATGTATATGATGAAAGCTTGTACTCTCT 858  
DB 1303 CACAGTTTCTCTCGAGTAACTGGCAGATGTATATGATGAAAGCTTGTACTCTCT 1362

QY 859 TTTTAAACCTCAAGTAACTCTGAGACAGATCACTAGATATTTTGAATTAATTAACAGCT 918  
DB 1363 TTTTAAACCTCAAGTAACTCTGAGACAGATCACTAGATATTTTGAATTAATTAACAGCT 1422

QY 919 CAGACTATTACAAATACACACCTGAAATAATGA 953  
DB 1423 CAGACTATTACAAATACACACCTGAAATAATGA 1457

RESULT 7

US-09-023-655-1004  
; Sequence 1004, Application US/09023655  
; Patent No. 6607879  
; GENERAL INFORMATION:  
; APPLICANT: Cocks, Benjamin G.  
; APPLICANT: Susan G. Stuart  
; APPLICANT: Jeffrey J. Seilhamer  
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE  
; TITLE OF INVENTION: EXPRESSION  
; NUMBER OF SEQUENCES: 1508  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
; STREET: 3174 PORTER DRIVE  
; CITY: PALO ALTO  
; STATE: CALIFORNIA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/023,655  
; FILING DATE: HEREWITH  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Zeller, Karen J.  
; REGISTRATION NUMBER: 37,071  
; REFERENCE/DOCKET NUMBER: PA-0001 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (650) 855-0555  
; TELEFAX: (650) 845-4166  
; INFORMATION FOR SEQ ID NO: 1004:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1599 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; LIBRARY: GENBANK  
; CLONE: g178325  
US-09-023-655-1004

Query Match 52.7%; Score 515.8; DB 3; Length 1599;  
Best Local Similarity 72.0%; Pred. No. 2.5e-136;  
Matches 673; Conservative 0; Mismatches 262; Indels 0; Gaps 0;

QY 19 AGAAGACAAATGAATGATTTGACATATTTGAACTACTAGTAAAGGCACTTTTGGGAAA 78  
DB 523 AAAGTGACCATGAATGACTTCGACTATCTCAAACCTCTTGGCAAGGGAACCTTTGGCAAA 582

QY 79 GTTATTTTGGTTCGAGAGAAGCAAGTGGAAATACTATGCTATGAAGATTTCTGAAGAAA 138  
DB 583 GTCATCTCTGGTGGGAGAGGCCACTGGCCGTACTACGCATGAAGATCTGCGAAG 642

QY 139 GAAGTCATTTATGCAAAAGATGAAGTGGCACACACTCTAACTGAAAGCAGAGATTTAAAG 198  
DB 643 GAAGTCATCTTGGCAAGGATGAAGTCGCTCACAGATCACCGAGAGCGGCTCTCCAG 702

QY 199 AACCTAGACATCCCTTTTAACTCTTTTAACTCTTTTAACTCTTTTAACTCTTTTAACTCTTTT 258  
DB 703 AACCTAGACATCCCTTTTAACTCTTTTAACTCTTTTAACTCTTTTAACTCTTTTAACTCTTTT 762

QY 259 TGTATTTGTGATGAATATGTTAAATGGGGCGGAGCTGTTTTCATTTGTCGAGAGAGCGG 318  
DB 763 TGTATTTGTGATGAATATGTTAAATGGGGCGGAGCTGTTTTCATTTGTCGAGAGAGCGG 822

QY 319 GTGTTCTCTGAGGACCGCACACGTTTCTATGTTGTCGAGAAATTTGTCCTGCTTGGACTAT 378



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; CURRENT APPLICATION NUMBER: US/09/417,197
; CURRENT FILING DATE: 1999-10-07
; NUMBER OF SEQ ID NOS: 143
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 138
; LENGTH: 2184
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: EGFP-PKB fusion
; NAME/KEY: CDS
; LOCATION: (1)..(2181)
US-09-417-197-138

Query Match      52.2%; Score 510.6; DB 3; Length 2184;
Best Local Similarity 72.5%; Pred. No. 8.5e-135;
Matches 676; Conservative 0; Mismatches 254; Indels 3; Gaps 1;

QY 24 GACATGAATGATTTTGACTATTGAAACTACTAGGTAAAGCAGCTTTTGGGAAAGTTAT 83
DB 1176 GACCATGAACGAGTTTGAGTACCTGAAGCTGTGGCAAGGCGACTTTTGGCAAGGTGAT 1235
QY 84 TTTGGTTTCGAGAGAAGGCAAGTGGAAATACATCTATGTAAGATCTCTGAAGAAAGT 143
DB 1236 CTGTGTGAAGGAAGGCGCACAGGCGCTACTACGCCATGAAGATCCTCAAGAAAGT 1295
QY 144 CATTATTGCAAAAGGATGAAGTGGCCACACACTCTAACTGAAAGCAGAGTATTAAAGAACAC 203
DB 1296 CATCTGTGGCCAGGAGGTGGCCACACACTCACCGAGAACCGGCTCTGCAGACTC 1355
QY 204 TAGACATCCCTTTTAAACATCTTGAATATCTTCCATTCAGACAAAGACCGTTTGTGTTT 263
DB 1356 CAGGCACCCCTTCTCCACAGCCCTGAAGTACTCTTTCCAGACCCACGACCGCTCTGCTT 1415
QY 264 TGTGATGGAATATGTTAATGGGGCGAGCTGTTTCCATTTGTCGAGAGCGGGTGT 323
DB 1416 TGTCTATGAGTACGCCAACGGGGCGAGCTGTTCTTCCACCTGTCCCGGGAACGTGTGT 1475
QY 324 CTCTGAGGACCCGACACACAGTTTCTATGGTGCAGAAATTTGTCTGCTTGGACTATCTACA 383
DB 1476 CTCGAGGACCGGGCCCGCTTCTATGGCGCTGAGATTGTGTGAGCCCTGGACTACTGCA 1535
QY 384 TTCGGAAGAAGA--TTGTGTACCGTGAATCTCAAGTTGGAGAAATCTAAATCTCGACAAAGA 440
DB 1536 CTCGAGAGAAGAAGCTGTGTACCGGACCTCAAGCTGGAGAACTCTATCTCGACAAAGA 1595
QY 441 TGGCCACATAAAATTTACAGATTTTGGACTTTTGCAGAGAGGATCACAGATGCGAGCCAC 500
DB 1596 CGGGCACATTAAGATCACAGACTTCGGGCTGTGCAAGGAGGGGATCAAGGACGGTGCAC 1655
QY 501 CATGAAGACATTTCTGTGGCACTCCAGAAATCTGCGCACAGAGGTGTTAGAAGATAATGA 560
DB 1656 CATGAAGACCTTTTGGCGGACACTGAGTACTTGGCCCCCGAGGTGCTGGAGGACATGA 1715
QY 561 CTATGCGCGAGCAGTAGACTGTGTGGGCGCTAGGGGTTGTCTATGTAATGATGTGGG 620
DB 1716 CTACGCGCGTGCAGTGAATCTGTGTGGGCTGTGGCGTGGTCTATGTACGAGATGATGTGG 1775
QY 621 GAGGTTACCTTTCTACAACACAGACCATGAGAAAATTTTTGAAATTAATTAATGAAGA 680
DB 1776 TCGCCTGCGCTTCTACAACACAGACCATGAGAAGCTTTTGTAGCTCATCTCATGAGGA 1835
QY 681 CATTAATTTCTCGAAACACTCTTTCAGATGCAAAATCATTTGCTTTCAGGGCTCTTGAT 740
DB 1836 GATTCGCTTCCCGCGCAGCGTGTGCTCCGAGGCCAAGTCTTGTCTTTTCAAGGCTGCTCAA 1895
QY 741 AAAGGATCCAAATAAAGCGCTTGTGGAGGACAGATGATGCAAAAGAAATATGAGACA 800
DB 1896 GAAGGACCCCAAGCAGAGGCTTGGCGGGGCTCCGAGGACGCAAGGAGATCATGACGA 1955
QY 801 CAGTTTCTTCTCTGGAGTAAATCGGCAAGATGATATATGATAAAAGCTTGTACCTCTT 860
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Db 1956 TCGCTTCTTTTGGCGGTATCGTGTGGCAGCAGCTGTACGAGAAGAGCTCAGCCACCCTT 2015
QY 861 TAAACCTCAAGTAACATCTGAGACAGATACCTAGATATTTTGTATGAAGAAATTTACAGTCA 920
DB 2016 CAAGCCCCAGGTCACGTCGGAGACTGACACACAGGTATTTTGTATGAGGAGTTTCAAGCCCA 2075
QY 921 GACTATTACAATTAACACACACCTGAAATAATGA 953
DB 2076 GATGATCACCATCACACACCTGACCAAGATGA 2108

RESULT 10
US-09-212-771-1
; Sequence 1, Application US/09212771
; Patent No. 5958773
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Lex M. Cowser
; TITLE OF INVENTION: ANTISENSE MODULATION OF AKT-1 EXPRESSION
; FILE REFERENCE: RTS-0034
; CURRENT APPLICATION NUMBER: US/09/212,771
; CURRENT FILING DATE: 1998-12-16
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 1
; LENGTH: 2610
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (199)..(1641)
US-09-212-771-1

Query Match      52.2%; Score 510.6; DB 2; Length 2610;
Best Local Similarity 72.5%; Pred. No. 9.2e-135;
Matches 676; Conservative 0; Mismatches 254; Indels 3; Gaps 1;

QY 24 GACATGAATGATTTTGACTATTGAAACTACTAGGTAAAGCAGCTTTTGGGAAAGTTAT 83
DB 633 GACCATGAACGAGTTTGAGTACCTGTAAGCTGTGGGCAAGGCGACTTTTCCGGAAGGTGAT 692
QY 84 TTTGGTTTCGAGAGAAGGCAAGTGGAAATACATCTATGAAGATTTCTGAAGAAAGAGT 143
DB 693 CTGTGTGAAGGAAGGCAAGGCGGCTACTACGCCATGAAGATCCTCAAGAGGAAGT 752
QY 144 CATTATTCAAAGGATGAAGTGGCAACACTCTAACTGAAAGCAGAGTATTAAAGAACAC 203
DB 753 CATCTGTGCAAGGACGAGGTGGCCACACACTACCGAGAACCGGCTCTCGACAGAACTC 812
QY 204 TAGACATCCCTTTTAAACATCTTGAATATTTCTTCCAGACAAAGACCGTTTGTGTTT 263
DB 813 CAGGCACCCCTTCTCTCACAGCCCTGAAAGTACTCTTTTCCAGACCCACGACCGCTCTGCTT 872
QY 264 TGTGATGAATATGTTAATGGGGCGAGCTGTTTTCATTTGTCGAGAGAGCGGTGTT 323
DB 873 TGTCTATGAGTACGCCAACGGGGCGAGCTGTTTCTTCCACCTGTCCCGGAACGTGTGTT 932
QY 324 CTCTGAGGACCGCACACACGTTTCTATGGTGCAGAAATTTGTCTGCTTGGACTATCTACA 383
DB 933 CTCGAGGACCGGGCCCGCTTCTATGGCGTGAGATTGTGTGAGCCCTGGACTACCTGCA 992
QY 384 TTCGGAAGAAGA--TTGTGTACCGTGAATCTCAAGTTGGAGAAATCTAAATCTCGACAAAGA 440
DB 993 CTCGAGAGAAGAAGCTGTGTGTACCGGACCTCAAGCTGGAGAACTCTATCTCGACAAAGA 1052
QY 441 TGGCCACATAAAATTTACAGATTTTGGACTTTTGAAGAGGAGGATCACAGATGCGAGCCAC 500
DB 1053 CGGGCACATTAAGATCACAGACTTCGGGCTGTGCAAGGAGGGGATCAAGGACGGTGCCAC 1112
QY 501 CATGAAGACATTTCTGTGGCACTCCAGAAATATCTGGCACCGAGAGGTGTTAGAAGATAATGA 560
DB 1113 CATGAAGACCTTTTGGGCGACACACTGAGTACTCTGCCCCCGAGGTTGCTGAGGAGCAATGA 1172
QY 561 CTATGCGCGAGCAGTAGACTGTGTGGGGCTTATGATGAAATGATGTGTGG 620
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Db 1173 CTACGGCGGTGACGTGGACTGTTGGGGCTGGGGCTGCTCATGTACGAGATGATGTGGG 1232  
Qy 621 GAGGTTACTCTTCTACAAACAGGACCATGAGAACTTTTGAATTAATTAATTAATGAAGA 680  
Db 1233 TCGGCTGCGCTTCTACAAACAGGACCATGAGAACTTTTGAAGCTCATCTCATGGAGGA 1292  
Qy 681 CATTAATAATTCCTCGAACACTCTCTTCAGATGCAAAATCAITGCTTTTCAGGGCTCTTGAT 740  
Db 1293 GATCGGCTTCCGCGCAGCTTGGTCCGAGGCCAAGTCCCTTCTTCAGGGCTGCTCAA 1352  
Qy 741 AAAGGATCCAAATAAAGCCCTTGGTGGAGGACAGATGATGCAAAAGAAATTAAGAGACA 800  
Db 1353 GAAGGACCCCAAGCAGAGGCTTGGCGGGGCTCCGAGGACCCCAAGGAGATCATGCAGCA 1412  
Qy 801 CAGTTTCTTCTCGAGTAAACTGCGAAGATGATATGATATAAAGCTTGACCTCTCTTT 860  
Db 1413 TCGCTTCTTTCGCGGTATCGTGTGGCAGCAGTGTACGAGAAAGCTTCAGCCCAACCTT 1472  
Qy 861 TAAACCTCAAGTAACATCTGAGACAGATCTAGATATTTTGAAGAAATTTACAGCTCA 920  
Db 1473 CAAGCCCGAGTCAAGTCCGAGACTGACACCAAGGTATTTTGAAGAGATTACGGCCCA 1532  
Qy 921 GACTATTACATAACACCACTGAAATATGA 953  
Db 1533 GATGATCACCATCACACCCTGACCAAGATGA 1565

## RESULT 11

US-09-081-058-1

; Sequence 1, Application US/09091058  
; Patent No. 6054285  
; GENERAL INFORMATION:  
; APPLICANT: Hemmings, Brian A.  
; APPLICANT: Frech, Matthias  
; TITLE OF INVENTION: Screening Method  
; FILE REFERENCE: 4-20683/A/20684/PCT  
; CURRENT APPLICATION NUMBER: US/09/091,058  
; CURRENT FILING DATE: 1998-06-10  
; EARLIER APPLICATION NUMBER: PCT/EP96/04814  
; EARLIER FILING DATE: 1996-11-05  
; EARLIER APPLICATION NUMBER: 9525703.6  
; EARLIER FILING DATE: 1995-12-15  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 2610  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (199)..(1641)

US-09-091-058-1

Query Match 52.2%; Score 510.6; DB 3; Length 2610;  
Best Local Similarity 72.5%; Pred. No. 9.2e-135;  
Matches 676; Conservative 0; Mismatches 254; Indels 3; Gaps 1;  
Qy 24 GACATGAATGATTTTGACTATTTGAAACTACTAGTTAAAGGCACTTTTGGGAAAGTTAT 83  
Db 633 GACCATGAACGAGTTTGAGTACCTGAAAGCTGCTGGCAAGGGCACTTTTCGGCAAGGTGAT 692  
Qy 84 TTTGGTTCGAGAGAGGCAAGTGAATACTATGCTATGAAGATCTGGAAGAAAGAT 143  
Db 693 CTGCTGAGAGAGAGGCGCAGCGGCTACTAGCCATGAGATCTCAGAGAGGAGT 752  
Qy 144 CATTAATGCAAGATGAAGTGGCACACACTCTAATCTGAAAGCAGAGATTTAAAGAACAC 203  
Db 753 CATCGTGGCCAAAGCAGAGGTGGGCCACACACTCACCGAGAACCGCTCTCGCAGAACTC 812  
Qy 204 TAGACATCCCTTTTAAACATCTTGAATATCTCTCCAGCAAAAGACCGTTTGTGTTT 263  
Db 813 CAGGACCCCTTCTCTACAGCCCTGAAAGTACTCTTTCCAGACCACCGACCGCTCTGCTT 872

Qy 264 TGTGATGGAATATGTTAATGGGGCGAGCTGTTTTTCCATTTGTGAGAGAGCGGGTGT 323  
Db 873 TGTGATGAGTACGCCAACGGGGCGAGCTGTTCTTCCACTGTCCCGGGAACGCTGTGT 932  
Qy 324 CTCTGAGGACCGCACAGCTTTCTATGTGAGAAATTTGTCTCTGCCCTTGGACTATCTACA 383  
Db 933 CTCGAGGACCGGGCCCGCTTCTATGGCGCTGAGATTGTGTACGCCCTGGACTACCTGCA 992  
Qy 384 TTCGGGAAGA---TTGTGTACCGTGTATCTCAAGTTGGAGAACTAATGCTGGCAAGA 440  
Db 993 CTCGGAAGAAACGTTGTGTACCGGGACCTCAAGCTGGAGAACCTCATGCTGGCAAGA 1052  
Qy 441 TGGCCACATAAAAATATACAGATTTTGGACTTTTCAAAAGAAAGGATCACAGATGACGCCAC 500  
Db 1053 CGGGCACATTAAGTACACAGACTTCGGGCTGTCAAGGAGGGATCAAGACGGTGGCCAC 1112  
Qy 501 CATGAAGACATCTGTGGCACTCCAGAAATATCTGGCAACGAGAGGTGTAGAAATATAGA 560  
Db 1113 CATGAAGACCTTTTGGCGCACACCTGAGTACCTGGCCCCCGAGGTGCTGGAGGACAATGA 1172  
Qy 561 CTATGGCCGAGCAGTAGACTGTTGGGGCTAGGGGTTGTATGATGAAATGATGTGTGG 620  
Db 1173 CTACGGCCGTGCAAGTGGAGCTGGGGCTGGGGCTGGTCAATGACGAGATGATGTGG 1232  
Qy 621 GAGGTTACCTTTCTACAAACGAGGACCATGAGAACTTTTGAATTAATTAATTAATGAAGA 680  
Db 1233 TCGGCTGCGCTTCTACAAACGAGGACCATGAGAGCTTTTGGAGCTCATCTCATGGAGGA 1292  
Qy 681 CATTAATAATTTCTCGAAACACTCTCTTCAGATGCAAAATCAATTTGTTTCAGGGCTCTTGAT 740  
Db 1293 GATCGGCTTCCGCGCACAGCTTGTTCGAGGCGCAAGTCTTGTCTTCAGGGCTGCTCAA 1352  
Qy 741 AAAGGATCCAAATAAAGCCCTTGGTGGAGGACAGATGATGCAAAAGAAATTAAGAGACA 800  
Db 1353 GAAGGACCCCAAGCAGAGGCTTGGCGGGGCTCCGAGGACCCCAAGGAGATCATGCAGCA 1412  
Qy 801 CAGTTTCTTCTCTGGAGTAAACTGGCAAGATGATATATGATAAAAGCTTTGTACCTCCTTT 860  
Db 1413 TCGCTTCTTTCGCGGTATCGTGTGGCAGCAGCTGTACGAGAGAAAGCTCAGCCCACTT 1472  
Qy 861 TAAACCTCAAGTAACTCTGAGACAGATCTAGATATTTTGAAGAAATTTTACAGCTCA 920  
Db 1473 CAAGCCCGAGTCAAGTCCGAGACTGACACCAAGGTATTTTGAAGAGATTACGGCCCA 1532  
Qy 921 GACTATTACATAACACCACTGAAATATGA 953  
Db 1533 GATGATCACCATCACACCCTGACCAAGATGA 1565

## RESULT 12

US-09-023-655-1206  
; Sequence 1206, Application US/09023655  
; Patent No. 6607879  
; GENERAL INFORMATION:  
; APPLICANT: Cocks, Benjamin G.  
; APPLICANT: Susan G. Stuart  
; APPLICANT: Jeffrey J. Seilhamer  
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE  
; TITLE OF INVENTION: EXPRESSION  
; NUMBER OF SEQUENCES: 1508  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
; STREET: 3174 PORTER DRIVE  
; CITY: PALO ALTO  
; STATE: CALIFORNIA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023,655
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1206:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2610 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: g190827
;
; US-09-023-655-1206

Query Match 52.2%; Score 510.6; DB 3; Length 2610;
Best Local Similarity 72.5%; Pred. No. 9,2e-135;
Matches 676; Conservative 0; Mismatches 254; Indels 3; Gaps 1;

QY 24 GACATGAATGATTTTGACTATTGAACTACTAGGTAAAGCACATTTTGGGAAAGTTAT 83
DB 633 GACCATGACGAGTTTGAGTACCTGAAGCTGTGGCAAGGCGACATTTGGGCAAGGTGAT 692
QY 84 TTTGGTTTCGAGAGAGGCAAGTGGAAATATCTATGCTATGAAGATTTCTGAAGAAAGT 143
DB 693 CCTGTGGAAGGAGAGGCGGCTACTACGCCATGAAGATCCTCAAGAAAGGAGT 752
QY 144 CATTTTGCAGAGATGAAGTGGGCACACACTTAATCTGAAGATTTCTGAAGAAAGT 203
DB 753 CATCGTGGCAAGGAGGCGGCTCACTCCGAGAACCCGCGCTCTCGAAGAACTC 812
QY 204 TAGACATCCCTTTTAAACATCTTGAATATTTCTTTCAGACAAAAGACCGTTTGTGTT 263
DB 813 CAGGCACCCCTTCCTCAGAGCCCTGAAGTACTCTTTTCAGACCCAGACCGGCTCTGCTT 872
QY 264 TGTGATGGAATATGTTAAATGGGGCGAGCTGTTTTTCCATTTTGTGCGAGAGCGGGTGT 323
DB 873 TGTCTATGAGTACGCCAACGCGGGCGAGCTGTTCTTCCACCTGTCCCGGAACGTTGT 932
QY 324 CTCTGAGGACCGCACACAGTTTCTATGTTGCGAAGAAATTTGTCTCTGCTTGGACTATCTACA 383
DB 933 CTCCGAGGACCGGGCCGCTTCTATGGGCGTGAAGATTTGTGTGAGGAACTCTGCTGCA 992
QY 384 TTCCGGGAAGA---TTGTGTACCGGTGATCTCAAGTTGGAGATCTAACTCTGACAAAGA 440
DB 993 CTCGAGAGAAACGCTGGTGTACCGGGACCTCAAGCTGGAGAACTCATGCTGGACAAAGA 1052
QY 441 TGGCCACATAAAATTTACAGATTTTGGACTTTGCAAGAGGAGGATCACAGATGCGAGCCAC 500
DB 1053 CCGGCACATTAAGATACAGATCTTGGGCTGTGCAAGAGGGGATCAAGGACGGTGGCCAC 1112
QY 501 CATGAAGACATTTCTGTGGCACTCCAGAAATATCTGGCACACAGAGGTGTTAGAAGATAATGA 560
DB 1113 CATGAAGACATTTTGGGGCACACCTGAGTACTTGGCCCCGAGGTGCTGGAGGACATGA 1172
QY 561 CTATGCGCAGAGTAGACTGTGTGGGCGCTAGGGGTGTGATGATGAAATGATGTGTGG 620
DB 1173 CTACGCGCGCTGAGTGAATGAGTGTGGGCGTGGGCGTGGTCAATGATACAGATGATGTGCG 1232
QY 621 GAGGTACTCTTTACAAACAGGACCATGAGAACTTTTGAATTAATTAATGGAAGA 680
DB 1233 TCGCCTGCCCCCTTCTACAAACAGGACCATGAGAACTTTTGTGAGCTCATCCTCATGAGGA 1292
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RESULT 13
US-09-590-740-1
; Sequence 1, Application US/09590740
; Patent No. 6689807
; GENERAL INFORMATION:
; APPLICANT: Kenneth Walsh
; APPLICANT: St. Elizabeth's Medical Center
; TITLE OF INVENTION: HMG CoA Reductase Inhibitors for
; TITLE OF INVENTION: Promoting Angiogenesis
; FILE REFERENCE: 49,784 (1417)
; CURRENT APPLICATION NUMBER: US/09/590,740
; CURRENT FILING DATE: 2000-06-08
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 2610
; TYPE: DNA
; ORGANISM: Homo sapiens
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; US-09-590-740-1
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Query Match 52.2%; Score 510.6; DB 3; Length 2610;
Best Local Similarity 72.5%; Pred. No. 9,2e-135;
Matches 676; Conservative 0; Mismatches 254; Indels 3; Gaps 1;

QY 24 GACATGAATGATTTTGACTATTGAACTACTAGGTAAAGCACATTTTGGGAAAGTTAT 83
DB 633 GACCATGACGAGTTTGAGTACCTGAAGCTGTGGCAAGGCGACATTTGGGCAAGGTGAT 692
QY 84 TTTGGTTTCGAGAGAGGCAAGTGGAAATATCTATGCTATGAAGATTTCTGAAGAAAGT 143
DB 693 CCTGTGGAAGGAGAGGCGGCTACTACGCCATGAAGATCCTCAAGAAAGGAGT 752
QY 144 CATTTTGCAGAGATGAAGTGGGCACACACTTAATCTGAAGATTTCTGAAGAAAGT 203
DB 753 CATCGTGGCAAGGAGGCGGCTCACTCCGAGAACCCGCGCTCTCGAAGAACTC 812
QY 204 TAGACATCCCTTTTAAACATCTTGAATATTTCTTTCAGACAAAAGACCGTTTGTGTT 263
DB 813 CAGGCACCCCTTCCTCAGAGCCCTGAAGTACTCTTTTCAGACCCAGACCGGCTCTGCTT 872
QY 264 TGTGATGGAATATGTTAAATGGGGCGAGCTGTTTTTCCATTTTGTGCGAGAGCGGGTGT 323
DB 873 TGTCTATGAGTACGCCAACGCGGGCGAGCTGTTCTTCCACCTGTCCCGGAACGTTGT 932
QY 324 CTCTGAGGACCGCACACAGTTTCTATGTTGCGAAGAAATTTGTCTCTGCTTGGACTATCTACA 383
DB 933 CTCCGAGGACCGGGCCGCTTCTATGGGCGTGAAGATTTGTGTGAGGAACTCTGCTGCA 992
QY 384 TTCCGGGAAGA---TTGTGTACCGGTGATCTCAAGTTGGAGATCTAACTCTGACAAAGA 440
DB 993 CTCGAGAGAAACGCTGGTGTACCGGGACCTCAAGCTGGAGAACTCATCCTCATGAGGA 1052
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Qy 441 TGGCCACATAAAATTACAGATTTTGGACTTTTGAAGTAAAGGAGGATCACAGATGAGCCAC 500
Db 1053 CGGACACATTAAAGATCAAGACTTCGGGCTGTGCAAGAGGGGATCAAGAGCGGTGCCAC 1112

Qy 501 CATGAAGACATTCTGTGGCACTCAGAAATATCTGGCACAGAGGTGTAGAAATATGA 560
Db 1113 CATGAAGACCTTTTTCGGGCACACCTGAGTACTTGGCCCCCGAGGTGCTGGAGGACAATGA 1172

Qy 561 CTATGGCGGAGCAGTACAGCTGGTGGGCGCTAGAGGTTGTATGATGAATGATGTGG 620
Db 1173 CTACGGCGGTGAGTGTGAGTGTGGGGCTGGGCGTGTGATGACGAGATGATGTGGG 1232

Qy 621 GAGGTTACCTTTCTCAACACAGGACCATGAGAAACTTTTGAATTAATATTAATGGAAGA 680
Db 1233 TCGCCTGCCCCCTTCTACAAACAGGACCATGAGAAGCTTTTGGAGTCACTCATCTCATGGAGGA 1292

Qy 681 CATTAATTTCTCGAACACTCTCTTCAGATGCAAAATCATTTGCTTCAGGGCTCTTGAT 740
Db 1293 GATCCGCTTCCCGGCGACGCTTGGTCCGAGGCCAAGTCTCTTGTCTTTCAGGGCTGTCTCAA 1352

Qy 741 AAAGGATCCAAATAAACGCCCTTGGTGGAGGACCATGATGCAAAAGAAATATGAGACA 800
Db 1353 GAAGGACCCCAAGCAGAGGCTTGGCGGGGCTCCGAGGACGCCAAGGAGATCATGCGACA 1412

Qy 801 CAGTTTCTTCTCTGGAGTAAACTGGCAAGATGATATATGATAAAAGCTTGTACCTCCTTT 860
Db 1413 TCGCTTCTTTCGGTGTGCTGGCAGCAGCTGTACGAGNAGAGCTCAGGCCACCTTT 1472

Qy 861 TAAACCTCAAGTAACATCTGAGACAGATATAGATATATTTGATGAAGAAATTTACAGCTCA 920
Db 1473 CAAGCCCCAGGTCAGCTGGAGACTGACACACAGGTATTTTGTAGGAGTTTACGGGCCA 1532

Qy 921 GACTATTACAAATAACACACCTGAAATATGA 953
Db 1533 GATGATCACCATCACACCCTGACCAAGATGA 1565

RESULT 14
US-09-590-740-3
; Sequence 3, Application US/09590740
; Patent No. 6689807
; GENERAL INFORMATION:
; APPLICANT: Kenneth Walsh
; APPLICANT: St. Elizabeth's Medical Center
; TITLE OF INVENTION: HMG CoA Reductase Inhibitors for
; TITLE OF INVENTION: Promoting Angiogenesis
; FILE REFERENCE: 49,784 (1417)
; CURRENT FILING DATE: 2000-06-08
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 1254
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-590-740-3

Query Match 50.4%; Score 493; DB 3; Length 1254;
Best Local Similarity 72.0%; Pred. No. 6.7e-130;
Matches 672; Conservative 0; Mismatches 255; Indels 6; Gaps 2;

Qy 24 GACAAATGAATGATTTGACTATTTGAACTACTAGGTAAAGGCACTTTTGGAAAGTTAT 83
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Qy 84 TTTGGTTTGGAGAGGCAAGTGGAAATATCTATGCTATGAAGATTTCTGAAGAAAGAAGT 143
Db 309 CCTGGTGAAGGAGAGGCCACAGCG---TACTACGCCATGAAGATCCTCAAGAGGAAGT 365

Qy 144 CATTTATGCAAGGATGAGTGGGACACACTCTAACTGAAAGCAGAGATTTAAAGACAC 203
Db 366 CATCGTGGCCAAAGGACGAGGTGGGCCACACACTACCGAGAAACCGCGTCCAGCAGAACTC 425
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Qy 204 TAGACATCCCTTTTAAACATCCTTTGAAATATTCCTTCCAGACAAAGACACCGTTTGTGTTT 263
Db 426 CAGGACCCCTTCTCTCACTCGCTGAGTACTCTTTCCAGACCCACGACCGCTCTGCTT 485

Qy 264 TGTGATGGAATATGTTAATGGGGCGAGCTGTTTTTCCATTTGTGAGAGAGCGGGTGT 323
Db 486 TGTATGGAGTAGCCCAACCGGGGCGAGCTGTTCTTCCACGTGTCGCGGAGCGTGTGTT 545

Qy 324 CTCTGAGGACCGCACAGTTTTCTATGTCGAGAAATGTCCTCTGCGCTTGGACTATCTACA 383
Db 546 CGCGAGGACCGGGCCGCTTCTATGGCGCTGAGATTGTGTGAGCCCTTGACTACCTGCA 605

Qy 384 TTCGGAAGA---TTGTGTACCGTGTATCTCAAGTTGGAGAATCTAATGTGGAACAAAGA 440
Db 606 CTGGAAGAAGACGTGTGTACCGGACCTCAAGCTGGAGAACCTCATGCTGGACAGGA 665

Qy 441 TGCGCACATAAATATACAGATTTTGACATTTGCAAAAGAGGATCACAGATGAGCCAC 500
Db 666 CGGACATTTAAGATCACAGACTTCGGGCTGTGCAAGGAGGGGATCAAGGACGGTGCAC 725

Qy 501 CATGAAGACATTCTGTGGCACTCCAGNAATATCTGGCACACAGAGGTGTAGAAATATGA 560
Db 726 CATGAAGACCTTTTGGCGGCACACTGAGTACTTGGCCCCCGAGGTGCTGAGGAGCAATGA 785

Qy 561 CTATGGCGGAGCAGTAGACTGGTGGGCTTAGGGTGTGTCATGTATGAAATGATGTGTGG 620
Db 786 CTACGGCGGTGAGTGGACTGTGTGGGGCTGGGGGTGTCATGTACGAGATGATGTGCGG 845

Qy 621 GAGGTTACCTTTTACAACACGAGACCATGAGAACTTTTGAATTAATATTAATGGAAGA 680
Db 846 TCGCCTGCCCTTCTCAAAACAGGACCATGAGAAAGCTTTTGTAGCTCATCTCATGGAGGA 905

Qy 681 CATTAATTTCTTCGAACACTCTTTCAGATGCAAAATCATTTGCTTTCAGGGCTCTTGAT 740
Db 906 GATCCGCTTCCCGGCACGCTTGGTCCGAGGCCAAGTCTCTTGTCTTTCAGGGCTGCTCAA 965

Qy 741 AAAGGATCCAAATAAACGCCCTTGGTGGAGGACCATGATGCAAAAGAAATTTATGAGACA 800
Db 966 GAAGGACCCCAAGCAGAGGCTTGGCGGGGCTCCGAGGACGCCAAGGAGATCATGCAGCA 1025

Qy 801 CAGTTTCTTCTCTGGAGTAAACTGGCAAGATGATATGATGATAAAAGCTTGTACCTCTTT 860
Db 1026 TCGCTTCTTTACCGGTATCGTGTGGCAGCAGCTGTACGAGAAGAGCTCAGCCACCCCTT 1085

Qy 861 TAAACCTCAAGTAACATCTGAGACAGATACTAGATATTTTGTGATGAAGAAATTTACAGCTCA 920
Db 1086 CAAGCCCCAGGTCAGCTCGGAGACTGACACCAAGTATTTTGTATGAGAGTTTACGGCCCA 1145

Qy 921 GACTATTACAAATAACACACCTGAAATATGA 953
Db 1146 GATGATCACCATCACACCACCTGACCAAGATGA 1178
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RESULT 15
US-09-474-922A-2
; Sequence 2, Application US/09474922A
; Patent No. 6187586
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Lex M. Cowser
; APPLICANT: Richard A. Roth
; TITLE OF INVENTION: ANTISENSE MODULATION OF Akt-3 EXPRESSION
; FILE REFERENCE: RTS-0036
; CURRENT FILING DATE: 1999-12-29
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 2
; LENGTH: 387
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-474-922A-2
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Query Match 39.2%; Score 383.8; DB 3; Length 387;  
Best Local Similarity 99.5%; Pred. No. 4.3e-99;  
Matches 385; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 557 ATGACTATGGCCGAGCAGTAGACTGGTGGGGCTAGGGGTTGTCATGTATGAAATGATGT 616  
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Db 1 ATGACTATGGCCGAGCAGTAGACTGGTGGGGCTAGGGGTTGTCATGTATGAAATGATGT 60  
|||  
QY 617 GTGGGAGGTTACTTTCTACAAACGAGGACCATGAGAAACTTTTTCGAATTAATTAATGG 676  
|||  
Db 61 GTGGGAGGTTACTTTCTACAAACGAGGACCATGAGAAACTTTTTCGAATTAATTAATGG 120  
|||  
QY 677 AAGACATTAAATTTCTCGAACACTCTCTTCAGATGCAAAATCAATGCTTTCAGGGCTCT 736  
|||  
Db 121 AAGACATTAAATTTCTCGAACACTCTCTTCAGATGCAAAATCAATGCTTTCAGGGCTCT 180  
|||  
QY 737 TGATAAAGGATCCAAATAAAACGCCCTTGGTGGAGGACCCAGATGATCAAAAAGAAATTATGA 796  
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Db 181 TGATAAAGGATCCAAATAAAACGCCCTTGGTGGAGGACCCAGATGATCAAAAAGAAATTATGA 240  
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QY 797 GACACAGTTTCTCTCTGGAGTAAACTGGCAAGATGTATATGATAAAAAGCTTGTACCTC 856  
|||  
Db 241 GACACAGTTTCTCTCTGGAGTAAACTGGCAAGATGTATATGATAAAAAGCTTGTACCTC 300  
|||  
QY 857 CTTTAAACCTCAAGTAACTCTGAGACAGATCTAGATATTTTCATGAAGNAATTACAG 916  
|||  
Db 301 CTCTTAAACCTCAAGTAACTCTGAGACAGATCTAGATATTTTCATGAAGNAATTACAG 360  
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QY 917 CTCAGACTATTACAATAACACCACCTG 943  
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Db 361 CTCAGACTATTACAATAACACCACCTG 387  
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Job time : 200 secs

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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 15, 2006, 06:06:54 ; Search time 259 Seconds  
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Title: US-10-601-311-2

Perfect score: 978

Sequence: 1 tctacaaccatcataaaag.....atggtatgactgcatgac 978

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 6247088 seqs, 457523669 residues

Total number of hits satisfying chosen parameters: 12494176

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications NA.New.\*

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- 2: /cgn2\_6/prodata/2/pubpna/US06\_NEW\_PUB.seq.\*
- 3: /cgn2\_6/prodata/2/pubpna/US07\_NEW\_PUB.seq.\*
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- 10: /cgn2\_6/prodata/2/pubpna/US11\_NEW\_PUB.seq.\*
- 11: /cgn2\_6/prodata/2/pubpna/US11\_NEW\_PUB.seq.\*
- 12: /cgn2\_6/prodata/2/pubpna/US60\_NEW\_PUB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	978	100.0	1547	6	US-10-826-585-45
2	861.4	88.1	1548	11	US-11-136-527-2956
3	525	53.7	1443	11	US-11-170-693-66
4	517	52.9	2349	11	US-11-136-527-2338
5	516.2	52.8	1617	11	US-11-136-527-1823
6	515.8	52.7	1715	7	US-10-947-249-56
7	401.8	41.1	600	11	US-11-136-527-7052
8	269.6	27.6	3201	11	US-11-136-527-4033
9	258.8	26.5	3206	7	US-10-821-234-306
10	253.6	25.9	2453	11	US-11-136-527-2486
11	246.4	25.2	3017	11	US-11-000-688-1184
12	236.4	24.2	2615	11	US-11-136-527-2878
13	229.8	23.5	5537	11	US-11-152-366-2
14	229.4	23.5	3075	11	US-11-136-527-1950
15	226.4	23.1	2146	7	US-10-955-054-34
16	223	22.8	3524	11	US-11-136-527-3329
17	222.4	22.7	2346	11	US-11-117-013-3
18	222.4	22.7	2346	11	US-11-000-688-1538
19	219	22.4	1800	11	US-11-136-527-3715
20	216.8	22.2	3186	7	US-10-995-561-339
21	216.8	22.2	3242	7	US-10-995-561-338

ALIGNMENTS

RESULT 1

US-10-826-585-45  
; Sequence 45, Application US/10826585  
; Publication No. US20060008807A1  
; GENERAL INFORMATION:  
; APPLICANT: Immunivest Corporation  
; APPLICANT: O'Hara, Shawn Mark  
; APPLICANT: Foulk, Brad  
; APPLICANT: Zweitzig, Daniel  
; TITLE OF INVENTION: Multiparameter analysis of comprehensive nucleic acids and  
; TITLE OF INVENTION: morphological features on the same sample  
; FILE REFERENCE: IMC 143 PCT/US  
; CURRENT APPLICATION NUMBER: US/10/826,585  
; CURRENT FILING DATE: 2004-04-16  
; PRIOR APPLICATION NUMBER: 60/369945  
; PRIOR FILING DATE: 2002-04-04  
; PRIOR APPLICATION NUMBER: 60/330669  
; PRIOR FILING DATE: 2002-11-26  
; PRIOR APPLICATION NUMBER: PCT/US02/26867  
; PRIOR FILING DATE: 2002-08-23  
; NUMBER OF SEQ ID NOS: 131  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 45

LENGTH: 1547  
TYPE: DNA  
ORGANISM: Human  
US-10-826-585-45

Query Match 100.0%; Score 978; DB 6; Length 1547;

Best Local Similarity 100.0%; Pred. No. 2.8e-260; Mismatches 0; Indels 0; Gaps 0;  
Matches 978; Conservative 0;

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Db	416	TCTACAACCCATCATATAAAGAAAGCAATGAATGATTTTGGTTGAGAGAAGGCAAGTGGAAAACTACTAGT	475
QY	61	AAAGGACCTTTTGGGAAAGTATTATTTGGTTGAGAGAAGGCAAGTGGAAAACTACTAGT	120
Db	476	AAAGGACCTTTTGGGAAAGTATTATTTGGTTGAGAGAAGGCAAGTGGAAAACTACTAGT	535
QY	121	ATGAAGATTCTGAAGAAAGAGTCAATTATTTGCAAGAGGATGAAGTGGCACAACCTCTAACT	180
Db	536	ATGAAGATTCTGAAGAAAGAGTCAATTATTTGCAAGAGGATGAAGTGGCACAACCTCTAACT	595

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Qy 181 GAAAGCAGAGTATTAAAGAACACATAGACATCCCTTTTAAATATATTCCTTC 240
Db 596 GAAAGCAGAGTATTAAAGAACACATAGACATCCCTTTTAAATATATTCCTTC 655
Qy 241 CAGACAAAGACCGTTTGTGTTTGTGATGGAATATGTTAATGGGGGAGCTGTTTTC 300
Db 656 CAGACAAAGACCGTTTGTGTTTGTGATGGAATATGTTAATGGGGGAGCTGTTTTC 715
Qy 301 CATTTGTGAGAGACCGGTTTCTCTGAGACCGCACACGTTTCTATGGTCGAGAAATT 360
Db 716 CATTTGTGAGAGACCGGTTTCTCTGAGACCGCACACGTTTCTATGGTCGAGAAATT 775
Qy 361 GTCTCTGCTTGGACTATCTACATTCGGAAGAAATGTTGTACCGTATCTCAAGTTGGAG 420
Db 776 GTCTCTGCTTGGACTATCTACATTCGGAAGAAATGTTGTACCGTATCTCAAGTTGGAG 835
Qy 421 AATCTAATGCTGGACAAAGATGGCCACATAAATAATACAGATTTTGGACATTGCAAGAA 480
Db 836 AATCTAATGCTGGACAAAGATGGCCACATAAATAATACAGATTTTGGACATTGCAAGAA 895
Qy 481 GGGATCAGATGCGACCCACATGAAGACATTTCTGTGGCACTCCAGAAATATCTGGCACCA 540
Db 896 GGGATCAGATGCGACCCACATGAAGACATTTCTGTGGCACTCCAGAAATATCTGGCACCA 955
Qy 541 GAGGTGTTAGAGATAATGACTATGCGCGAGCAGTAGACTGGTGGGCGCTAGGGGTTGTC 600
Db 956 GAGGTGTTAGAGATAATGACTATGCGCGAGCAGTAGACTGGTGGGCGCTAGGGGTTGTC 1015
Qy 601 ATGTATGAATGATGTGGGAGGTTACCTTTCTCAACCGGACCATGAGAACTTTTT 660
Db 1016 ATGTATGAATGATGTGGGAGGTTACCTTTCTCAACCGGACCATGAGAACTTTTT 1075
Qy 661 GAAATTAATTAATGGAAGACATTAATTTCTCGAACACTCTCTCAGATGCAAAATCA 720
Db 1076 GAAATTAATTAATGGAAGACATTAATTTCTCGAACACTCTCTCAGATGCAAAATCA 1135
Qy 721 TTGCTTTTCAGGCTCTTGATAAAGGATCCAAATAAACGCCCTTGTGGAGCACCATGAT 780
Db 1136 TTGCTTTTCAGGCTCTTGATAAAGGATCCAAATAAACGCCCTTGTGGAGCACCATGAT 1195
Qy 781 GCAAAAGAAATATGAGACACAGTTTCTCTCGAGTAACTGGCAAGATGATATGAT 840
Db 1196 GCAAAAGAAATATGAGACACAGTTTCTCTCGAGTAACTGGCAAGATGATATGAT 1255
Qy 841 AAAAGCTTGTACCTCTTTTAAACCTCAAGTAACTCTGAGACAGATACCTAGATATTTT 900
Db 1256 AAAAGCTTGTACCTCTTTTAAACCTCAAGTAACTCTGAGACAGATACCTAGATATTTT 1315
Qy 901 GATGAAGAAATTTACGCTCAGACTATTACAAATAACACACCTGAAATAATGATGAGGAT 960
Db 1316 GATGAAGAAATTTACGCTCAGACTATTACAAATAACACACCTGAAATAATGATGAGGAT 1375
Qy 961 GGTATGACTCGATGGAC 978
Db 1376 GGTATGACTCGATGGAC 1393
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RESULT 2

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US-11-136-527-2956
; Sequence 2956, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136.527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2956
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; LENGTH: 1548
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-2956
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Query Match 88.1%; Score 861.4; DB 11; Length 1548;
Best Local Similarity 94.1%; Pred. No. 4.5e-228;
Matches 895; Conservative 0; Mismatches 56; Indels 0; Gaps 0;
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Qy 1 TCTACACCCCATCATAAAGAAAAGACAAATGAATGATTTTGACATATTTGAAACTACTAGGT 60
Db 452 TCTACACCCCATCATAAAGAAAAGACAAATGAATGATTTTGACATATTTGAAACTACTAGGT 511
Qy 61 AAAGGCACCTTTTGGGAAAGTTATTTTGGTTCGAGAGAAAGCAAGTGGAAATATCTATGCT 120
Db 512 AAAGGCACCTTTTGGGAAAGTTATTTTGGTTCGAGAGAAAGCAAGTGGAAATATCTACGCT 571
Qy 121 ATGAGATTTCTGAAGAAAAGTCAATATTTGCAAGGATGAAGTGGCACACTCTAAT 180
Db 572 ATGAGATTTCTGAAGAAAAGTCAATATTTGCAAGGATGAAGTGGCACACTCTAAT 631
Qy 181 GAAAGCAGAGTATTTAAAGAACACTTAGACATCCCTTTTAAATGAAATATTTCTCTTC 240
Db 632 GAGAGCAGAGTCTTAAAGAACACACAGACATCCATTTCTAAATCCTTTGAAATATTTCTTC 691
Qy 241 CAGACAAAAGACCGTTTGTGTTTGTGATGGAATATGTTAATGGGGCGAGCTGTTTTTC 300
Db 692 CAGACAAAAGACCGTTTGTGTTTGTGATGGAATATGTTAATGGGGCGAGCTGTTTTTC 751
Qy 301 CATTTGTGAGAGACGGGTTTCTCTGAGGACCGCACACGTTTCTATGGTCGAGAAATT 360
Db 752 CATTTGTGAGAGACGGGTTTCTCTGAGGACCGCACACGTTTCTATGGTCGAGAAATT 811
Qy 361 GTCTCTGCTTGGACTATCTACATTTCCGGAAGATGTTGTACCGTATCTCAAGTTGCGAG 420
Db 812 GTCTCTGCTTGGACTATCTACATTTCCGGAAGATGTTGTACCGTATCTCAAGTTGCGAG 871
Qy 421 AATCTAATGCTGCAAAAGATGGCCACATATAAATAATACAGATTTTGGACTTTTGCAGAA 480
Db 872 AATCTAATGCTAGATAAGGATGGCCATATAAATAATACGATTTTGGACTTTTGCAGAA 931
Qy 481 GGGATCAGATGCGACCCACATTAAGACATTTCTGTGGCACTCCAGAAATATCTGGCACCA 540
Db 932 GGGATCAGATGCGACCTACCATGAAGACATTTCTGTGTTACACCCAGAGTATCTGGCACCA 991
Qy 541 GAGGTGTTAAGATAATGACTATGCGCGAGCAGTAGACTGGTGGGCGCTAGGGGTTGTC 600
Db 992 GAGGTATTAAGATAATGACTATGCGCGAGCAGTAGACTGGTGGGCGCTAGGGGTTGTC 1051
Qy 601 ATGTATGAATGATGTTGGGAGGTTTACCTTTTCTCAACCCAGGACCATGAGAACTTTT 660
Db 1052 ATGTATGAATGATGTTGGGAGGTTTACCTTTTCTCAACCCAGGACCATGAGAACTTTT 1111
Qy 661 GAATTAATTAATGGAAGACATTAATTTCTCGAAACACTCTCTTCAGATGCAAAATCA 720
Db 1112 GAATTAATTAATGGAAGACATTAATTTCTCGAAACACTCTCTTCAGATGCAAAATCA 1171
Qy 721 TTGCTTTTCAGGCTCTTGATAAAGGATCCAAATAAACGCCCTTGTGGAGCACCATGAT 780
Db 1172 TTGCTTTTCAGGCTCTTGATAAAGGATCCAAATAAACGCCCTTGTGGAGGCGCCAGAT 1231
Qy 781 GCAAAAGAAATTTAGACACAGTTTCTCTCTGGAGTAAACTGGCAAGATGATATATGAT 840
Db 1232 CCAAGAGATATAGGACACAGTTTCTTTCTGGAGTAACTGGCAGGACGATATATGAC 1291
Qy 841 AAAAGCTTGTACTCTCTTTTAAACCTCAAGTAACTCTGAGACAGATATCTAGATATTT 900
Db 1292 AAAAGCTTGTACTCTCTTTTAAAGCTCAAGTAACTCTGAGACAGACACAGATATTT 1351
Qy 901 GATGAAGAAATTTACAGCTCAGCTATTTACAAATACACCCACTGAAATAT 951
Db 1352 GATGAAGAAATTTACAGCTCAGCTATTTACAAATACACCCACTGAAAGTGT 1402
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RESULT 3
US-11-170-693-66
; Sequence 66, Application US/111170693
; Publication No. US20060014186A1
; GENERAL INFORMATION:
; APPLICANT: Hodge, Timothy A.
; TITLE OF INVENTION: METHODS FOR GENOTYPE SCREENING OF A STRAIN DISPOSED ON AN
; FILE OF INVENTION: ABSORBENT CARRIER
; FILE REFERENCE: 023131.41500
; CURRENT APPLICATION NUMBER: US/11/170,693
; CURRENT FILING DATE: 2005-06-29
; PRIOR APPLICATION NUMBER: 60/230,371
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 09/945,952
; PRIOR FILING DATE: 2001-09-04
; PRIOR APPLICATION NUMBER: 11/074,995
; PRIOR FILING DATE: 2005-03-08
; PRIOR APPLICATION NUMBER: 11/
; PRIOR FILING DATE: 2005-06-24
; NUMBER OF SEQ ID NOS: 73
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 66
; LENGTH: 1443
; TYPE: DNA
; ORGANISM: Mus sp.
US-11-170-693-66

Query Match      53.7%; Score 525; DB 11; Length 1443;
Best Local Similarity 73.4%; Pred. No. 3.5e-135;
Matches 685; Conservative 0; Mismatches 245; Indels 3; Gaps 1;

QY 24 GACAAATGAATGATTTTGACTATTGAACTACTAGGTAAAGGCACCTTTTGGGAAAGTTAT 83
DB 435 GACCATTGAACGAGTTTGACTGAACTACTGGCAAGGCACCTTTGGGAAAGTTAT 494
QY 84 TTTGGTTCAGAGAGAGGCAAGTGGAAATACTATGCTATGAAGATCTCGAAGAAAGAT 143
DB 495 TCTGGTGAAGAGAGAGGCAAGTGGCAAGTCTATGCTATGCAAGATCTCAAGAAAGGAT 554
QY 144 CATTATTGCAAGAGGATGAAGTGGCACACACTCTAACTGAAAGCAGAGTATTAAAGAACAC 203
DB 555 CATGTGCGCAAGGATGAGTTGCGCACACAGCTTACTGAGAACCGTGTCTCGAAGAACATC 614
QY 204 TAGACATCCCTTTTAACTATCTTGAATATCTCTTCCAGACAAAGACCGTTTGTGTTT 263
DB 615 TAGGCATCCCTTCTTACGCGCTCAAGTACTCATTTCCAGACCCACGCGCTCTGTCTT 674
QY 264 TGTGATGGAATATGTTAAATGGGGGCGAGCTGTTTTCCTATTTGTCAGAGAGCGGGTGT 323
DB 675 TGTGATGGAATATGTTAAATGGGGGCGAGCTGTTTTCCTATTTTCAGAGAGCGGGTGT 734
QY 324 CTCTGAGGACCGCACACGTTTCTATGTCGCAAAATGTTCTGCTGCTTGGACTATCTACA 383
DB 735 CTCGAGGACCGGGCGCGCTTCTATGTCGCGAGATTTGTCTGCTTGGACTATCTGCA 794
QY 384 TTCCGGAAGA---TTGTGTACCGTATCTCAAGTTGGGAATCTAAATCTCGACAAAGA 440
DB 795 CTCGAGAGAGACGTTGTGTACCGGACCTGAAGCTGGAGACCTCATCTCGACAAAGA 854
QY 441 TGCCCAATAAAATTAAGATTTTGGACTTTTGAATTTTGAATTTTGAAGAGGATCAGATGCAAGCCAC 500
DB 855 CGGGACATCAAGATAACGACTTCGGGCTGTGCAAGAGGGGATCAAGAGATGTTGCCAC 914
QY 501 CATGAGACATTTGTGGCACTCCAGAAATCTGGCACGAGAGGTTTGAAGAGATATGA 560
DB 915 TATGAAGACATTTCTGGGAAACCGCGAGTACTTGGCGCTTGGAGTGTCTGGAGAACCA 974
QY 561 CTATGCGCGAGAGTATGATGTTGGGCGCTTAGGGGTTGTCTATGAAATGATGTGG 620
DB 975 CTACGCGCGTGCAGTGCATGTTGGGGGCTTGGCGTGTGTCATGATGATGATGTGG 1034
QY 621 GAGGTTACCTTTCTACAAACGAGCCATGAGAAACCTTTTGAATTAATTAATGAAGA 680

RESULT 4
US-11-136-527-2338
; Sequence 2338, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2338
; LENGTH: 2349
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-2338

Query Match      52.9%; Score 517; DB 11; Length 2349;
Best Local Similarity 71.3%; Pred. No. 6.8e-133;
Matches 667; Conservative 9; Mismatches 259; Indels 0; Gaps 0;

QY 19 AGAAAGACAATGAATGATTTTGACTATTGAACTACTAGGTAAAGGCACCTTTTGGGAAA 78
DB 717 AAAGTGACCATGAACGACTTCGATTTATCTCAAACTCTCGGCAAGGGCACCTTTCGGCAA 776
QY 79 GTTATTTTGGTTCGAGAGAGGCAAGTGGAAATACTATGCTATGAGATTTCTGAGAAA 138
DB 777 GTTATTTTGGTTCGAGAGAGGCAAGTGGAAATACTATGCTATGAGATTTCTGAGAAA 836
QY 139 GAAGTCATTATTGCAAGGATGAAGTGGCACACACTCTAACTGAAAGCAGAGATTTAAAG 198
DB 837 GAGGTATCATTTGCAAGGATGAAGTGGCCACACAGTCACAGAGAGCGAGTCTTACAG 896
QY 199 AACACTAGACATCCCTTTTAAATCATCTTGTGAATATTTCTTCCAGACAAAGACCGTTTG 258
DB 897 AATACAGGACCCCTTTCCTTACAGCCCTGAAAGTATGCCCTTCAGACCCCATGACCCGCTG 956
QY 259 TGTGTTGATGGAATATGTTAAATGGGGCGAGCTGTTTTCCTATTTGTCAGAGAGCGG 318
DB 957 TGTGTTGATGGAATATGTTAAATGGGGCGAGCTGTTTTCCTATTTGTCAGAGAGCGG 1016
QY 319 GTGTTCTCTGAGGACCGCACACGTTTCTATGTCGCAAAATTTGTCTGCTTGGACTAT 378
DB 1017 GTCTTACGAGGATCGGGCACGCTTTTATGTCGAGAGATTTGTGTCAGTCTGTCGAGTAC 1076
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Qy 379 CTACATTCGGAAAGATTGTGTAACGTTGATCTCAAGTTGGAGAAATCTAATGCTCGACAAA 438  
Db 1077 TTGCACTCGASGGATGTGGTGTACCGGACATCAAGCTGGAAAACCTTATGCTGGACAAA 1136  
Qy 439 GATGCCACATAAAATTTACAGATTTGGACTTTGCAAGGAGGATCACAGATGCGAGCC 498  
Db 1137 GATGGCCACATCAAGATCACGTGACTTTGGCTTTGSCAAAGAGGCGATCAGTGATGGGGCC 1196  
Qy 499 ACCATGAAGACATCTGTGGCACTCCAGAAATATCTGGCACCAGAGGTGTTAGAAAGATAAT 558  
Db 1197 ACCATGAAGAACTTSTGTGTACCCCGAGTACTTTGGCGCTGAGGTGCTAGAGACAAAT 1256  
Qy 559 GACTATGCCAGCAGATAGACTGTGGGGCTTAGGGGTTCATGTATGAATGATGTGT 618  
Db 1257 GAMTACGGGCGTGAGTGGACTGTGGGACTGGGCGTGGTTCATGTACGAGATGATGTGC 1316  
Qy 619 GGGAGGTTACCTTTCTACAAACGAGGACCATGAGAACTTTTGAATTAATTAATGAA 678  
Db 1317 GGCGGCTGCGCTTCTACAAACGAGGACCAAGAGCGCTCTTCGAGCTCATCCTCATGGAG 1376  
Qy 679 GACATTAATTTCTCGAACTCTCTTCAGATGCAAAATCATTTGCTTCAGGGCTCTTG 738  
Db 1377 GAGATCGGTTCCACGACGCTTTGGCCAGAGGCGAAGTCCCTGCTGGCTGGACTGCTC 1436  
Qy 739 ATAAAGATCCAAATAAACGCTTTGGTGAGGACAGATGATGCAAAAGAAATTTATGAGA 798  
Db 1437 AAGAAGACCCYAAGCAGAGGCTCGTGGGGGTCCAGTGATGMAAGGAGGTCAATGGAG 1496  
Qy 799 CACAGTTTCTCTCGAGTAAACTGGCAAGATGTATATGATAAAGCTTGTACCTCCT 858  
Db 1497 CATCGGTTCTTCTCAGCATCAACTGGCAGGATGTGGTACAGAAAGAGCTCCTGCCACCC 1556  
Qy 859 TTTAAACCTCAAGTAACATCTGAGACAGATACTAGATATTTTGATGAAGAAATTTACAGCT 918  
Db 1557 TTCAAACCTCAGGTCACTTCAGAGTGGACAAAGGTACTTTGATGATGAATTCACCGCC 1616  
Qy 919 CAGACTATTACAATAACACCACTCTGAAAATATGA 953  
Db 1617 CAGTCCATCAATACACACCCCGACCGCATATGA 1651  
RESULT 5  
US-11-136-527-1823  
; Sequence 1823, Application US/11136527  
; Publication No. US20050287570A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes  
; FILE REFERENCE: 031896-041000 (AM101086)  
; CURRENT APPLICATION NUMBER: US/11/136,527  
; CURRENT FILING DATE: 2005-05-25  
; PRIOR APPLICATION NUMBER: US 60/574,294  
; PRIOR FILING DATE: 2005-05-26  
; NUMBER OF SEQ ID NOS: 362830  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 1823  
; LENGTH: 1617  
; TYPE: DNA  
; ORGANISM: Rattus norvegicus  
US-11-136-527-1823  
Query Match 52.8%; Score 516.2; DB 11; Length 1617;  
Best Local Similarity 71.7%; Pred. No. 9.9e-133;  
Matches 669; Conservative 14; Mismatches 247; Indels 3; Gaps 1;  
Qy 24 GACAATGAATGATTTGACTATTTGAAACTACTAGTAAAGGCATCTTTTGGGAAAGTTAT 83  
Db 477 GACCATGAACGAGTTTGATACCTGAGCTACTGGCAAGGGCACCTTTTGGGAAGGTGAT 536  
Qy 84 TTTGGTTCAGAGAGGCAAGTGAATACTATGCTATGAAGATTTCTGAAGAAAGAT 143  
Db 537 CCTGGTGAAGGAGAGGCCACAGGTTCGCTACTATGCCATGAAGATTCCTCAAGAAAGGAGGT 596

Qy 144 CATTTATGCAAGGATGAAGTGGCACACACTCTAACTGAAAGCAGAGTATTAAAAAGACAC 203  
Db 597 CATCGTTGCCAAGATGAGGTGGCCACACCGTTACTGAGAACCGTGTCTCGCAGAACTC 656  
Qy 204 TAGACATCCCTTTTAAATCATCTTTGAAATATTCCTTCAGACAAAAGACCGTTTGTGTGT 263  
Db 657 TAGGCATCCCTTCTTACAGCCCTCAAGKACTCATTCAGACCCACGACCCCTCTGTT 716  
Qy 264 TGTGATGGAATATGTTAATGGGGCGAGCTGTTTTTCCATTTGTCGAGAGACGGGTGTT 323  
Db 717 TGTGATGAGTACGCCAATGGGGCGAGCTCTTCTTTCACCTGTCTCGTGAGCGGTGTT 776  
Qy 324 CTCTGAGGACCGCACACAGCTTTCTATGTCGAGAAATTTCTCTGCCCTTGGACTATCTACA 383  
Db 777 TTCAGAGGACCGGGCCCGCTTCTACGTCGGAGATTTGTGTCGCCCTCGACTACTTGCA 836  
Qy 384 TTCCGGAAGA---TTGTGTACCGTGATCTCAAGTTGGAGAAATCTAATGTCGGACAAAGA 440  
Db 837 CTCGGAAGAAACGTCGTGTACCGGGACCTCAAGCTGGAGAACTCATGCTGGACAAGGA 896  
Qy 441 TGCCCATAAATTTACAGATTTTGACCTTTGCAAGAGGGATCACAGATGCGAGCCAC 500  
Db 897 CGGGCACTCAAGATAACGGACTTCKGGCTGTGCAAGAGGGTATCAAGGACGGTGCAC 956  
Qy 501 CATGAAGACATTTCTGTGGCACTCCAGAAATATCTGGCACACAGAGGTGTTAGAAAGATAATGA 560  
Db 957 CATGAAGACGTTCTGTGGGACACCCGAGTACCTGGCCGTCGAGGTGCTGGAGGACNACGA 1016  
Qy 561 CTATGGCCGAGCAGTAGACTGTGGGGCCCTAGGGGTTGTCAATGATGAATGATGTGTGG 620  
Db 1017 CTATGGCCGTCAGTGGACTGTGGGGCTGGGCGTGTGATGATGATGATGATGTCGG 1076  
Qy 621 GAGGTACCTTTCTACACAGGACCATGAGAACTTTTGAATTAATTAATTAATGAGAGA 680  
Db 1077 CCGCTGCCCTTCTACAAACGAGGACCATGAGAACTGTTCGAGCTCATCTTAATGGAGGA 1136  
Qy 681 CATTAATAATTTCTCGAAACACTCTCTTCAGATGCAAAAATCATTTGCTTTTCAGGGCTCTTGAT 740  
Db 1137 GATCCGCTTCYACGCAYACTCGGGCCGAGGCCAAGTCCCTGCTCTCGGGGCTGCTCAA 1196  
Qy 741 AAAGGATCCAAATAAACCCCTTGTGGAGGACACAGATGATGCAAAAAGAAATTTAGAGACA 800  
Db 1197 GAASGACCTTACACAGAGGCTCGGTGGGGCTCGCAKAGCCCAWKAGAGATCATGACGA 1256  
Qy 801 CAGTTTCTCTCTCGAGTAACTGGCAAGATGTATATGATAAAGCTTGTACCTCCTTT 860  
Db 1257 CCGCTTCTTTGCCAAACATCGTGTGGCAAGATGTGTATGAGAAAGCTGAGCCACCTTT 1316  
Qy 861 TAAACCTCAAGTAACATCTGAGACAGATAGATATTTTGAATGAAGAAATTTACAGCTCA 920  
Db 1317 CAAGCCCCAGTCACTCTGAGACCGACACCGGTATTTTGTATGAGGAGTTTACAGCTCA 1376  
Qy 921 GACTATTACAAATACACCACCTGAAAATATGA 953  
Db 1377 GATGATVACCATCACRYCGCTGATYAAGATGA 1409  
RESULT 6  
US-10-947-249-56  
; Sequence 56, Application US/10947249  
; Publication No. US20050287541A1  
; GENERAL INFORMATION:  
; APPLICANT: Akira NAKAGAWARA  
; APPLICANT: Miki OHIRA  
; APPLICANT: Shin ISHII  
; APPLICANT: Takeshi GOTO  
; APPLICANT: Hiroyuki KUBO  
; APPLICANT: Takahiro HIRATA  
; APPLICANT: Yasuko YOSHIDA  
; APPLICANT: Saichi YAMADA  
; TITLE OF INVENTION: Microarray for Predicting the Prognosis of Neuroblastoma and Meth  
; TITLE OF INVENTION: Predicting the Prognosis of Neuroblastoma

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; FILE REFERENCE: 117007
; CURRENT APPLICATION NUMBER: US/10/947,249
; CURRENT FILING DATE: 2004-09-23
; PRIOR APPLICATION NUMBER: US 60/505,614
; PRIOR APPLICATION NUMBER: 2003-09-25
; NUMBER OF SEQ ID NOS: 200
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 56
; LENGTH: 1715
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-947-249-56

Query Match      52.7%; Score 515.8; DB 7; Length 1715;
Best Local Similarity 72.0%; Pred. No. 1.3e-132;
Matches 673; Conservative 0; Mismatches 262; Indels 0; Gaps 0;

QY 19 AGAAGACCAATGAATGATTTCGACTATTGAACTACTAGGTAAGGACCTTTTGGGAAA 78
DB 639 AAAGTGACCATGAATGACTTCGACTATCTCAAACTCCTTGGCAAGGAACCTTTGGCAAA 698

QY 79 GTTATTTTGGTTCGAGAGAGCAAGTGGAAATACTATGCTATGAAGATTCTGAAGAAA 138
DB 699 GTCATCTCTGGTGGGAGAGAGCCACTGGCGCTACTAGCCCATGAAGATCCTGGGAAAG 758

QY 139 GAAGTCATTATTGCAAGAGTGAAGTGGCAACACTCTAACTGAAAGCAGAGATTATTAAG 198
DB 759 GAAGTCATCATTTGCCAAGGATGAAGTCGCTCACAGACTCAGCGAGAGCGGGTCTCCAG 818

QY 199 AACACTAGACATCCCTTTTAAATCATCTTGAATATCTTCCACACAAAGACCGTTTG 258
DB 819 AACACAGGACCCGTTCTCTACTCGCTGGAAGTATGCCCTCCAGACCCAGCCGCTG 878

QY 259 TGTATTTGATGGAATATGTTAATGGGGCGAGCTGTTTTCCATTGTTCGAGAGAGCGG 318
DB 879 TGCTTTGTGATGAGTATGCAACGGGGGTGAGCTGTTCTTCCACTGTCCCGGAGCGT 938

QY 319 GTGTTCTCTGAGGACCGCACAGTCTTCTATGTTGTCAGAAATTTGCTCTGCGCTTGACTAT 378
DB 939 GTCTTTCACAGAGAGCGGGCCCGGTTTTATGTTGTCAGAGATTGTCTCGGCTCTTGATAC 998

QY 379 CTACATTCGGAAAGATTTGTGTACCGTGTATCTCAAGTTGGAGAACTAATCTGTCGACAAA 438
DB 999 TTGCACTCCGGGAGCGTGTGTATACCGCGACATCAAGCTGGAAACCTCATGCTGACAAA 1058

QY 439 GATGCGCACATAAAATTTACAGATTTTGACATTTGCAAAAGAGGATCACAGATGCAGCC 498
DB 1059 GATGCGCACATCAAGATCACTGACTTTGGCCTCTGCNAAGAGGCGATCAGTGACCGGGCC 1118

QY 499 ACCATGAAGACATTTCTGTGGCACTCCAGAAATATCTGGCACCAAGAGGTGTAGAAGATAAT 558
DB 1119 ACCATGAAGAACCTTCTGTGGGACCCCGAGTAGTACCTGGCGCCTGTGAGGTGTGGAGACAAT 1178

QY 559 GACTATGGCCGAGCAGTACAGTGTGGGCGCTAGGGCTGTGTCATCTATGAATGATGTGT 618
DB 1179 GACTATGGCCGCGCGCTGTGACTGTGGGGGCTGGGTGTGTCATCTATGAATGATGTGTG 1238

QY 619 GGGAGGTTACCTTTCTACACAGGACCATGAGAAATCTTTTGAATTAATATTAATGAA 678
DB 1239 GGGCGCTGCGCTTTCTACACAGGACCCAGAGCGCCTCTTCGAGCTCATCTCATGAGAA 1298

QY 679 GACATTAATTTCTCGAACAATCTCTCTTCAGATGCAAAATATCATTTGTTTCAGGGCTCTTG 738
DB 1299 GAGATCCGCTTCCCGCGCAGCTCAGCCCGGAGGCAAGTCCCTGCTTCTGGGCTGCTT 1358

QY 739 ATAAAGGATCCAAATAAAACCTTTGGTGGAGGACAGATGATGCAAAAGAAATTAATGAGA 798
DB 1359 AAGAAGGACCCCAAGCAGAGGCTTGGTGGGGGGCCCGAGCGATGCCAAGAGGCTCATGGAG 1418

QY 799 CACAGTTTCTCTCTGAGCTAAACTGGCAAGATGTATATGATAAAAGCTTTGACTCTCT 858
DB 1419 CACAGTTTCTCTCTGAGCTAACTGGCAGGACGTGGTCCAGAGAGCTCTCTGCCACCC 1478

; FILE REFERENCE: 117007
; CURRENT APPLICATION NUMBER: US/10/947,249
; CURRENT FILING DATE: 2004-09-23
; PRIOR APPLICATION NUMBER: US 60/505,614
; PRIOR APPLICATION NUMBER: 2003-09-25
; NUMBER OF SEQ ID NOS: 200
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 57
; LENGTH: 1715
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-7052

Query Match      41.1%; Score 401.8; DB 11; Length 600;
Best Local Similarity 92.9%; Pred. No. 2.7e-101;
Matches 421; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

QY 499 ACCATGAAGACATTTCTGTGGCACTCCAGAATATCTGGCACCAAGAGGTGTGAAGATAAT 558
DB 2 ACCATGAAGACATTTCTGTGTACACCAGAGTATCTGGCACCAAGAGGTATTAGAAGATAAT 61

QY 559 GACTATGGCCGAGCAGTACAGTGTGGGCGCTAGGGCTGTGTCATGTATGAAATGATGTGT 618
DB 62 GACTATGGCCGAGCTGTGGACTGTGGTGGGCGCTAGGTGTGTCATGTATGAAATGATGTGT 121

QY 619 GGGAGGTTACCTTTCTACACAGGACCATGAGAACTTTTGAATTAATTAATGAGAA 678
DB 122 GGGAGGTTGCGCTTTCTACACAGGAGATCATGAGAACTCTTTGAACTAATACTCATGGAA 181

QY 679 GACATTAATTTCTCTCGAACAATCTCTTTCAGATGCAAAATCATTTCTTTCAGGGCTCTTG 738
DB 182 GACATCAAAATTTCCCGGCAACACTCTCTTTCAGATGCAAAAGTCAATGCTTTCAGGGCTCTTG 241

QY 739 ATAAAGGATCCAAATAAAACGCTTTGGTGGAGGACAGATGATGCAAAAGAAATTAATGAGA 798
DB 242 ATAAAGGATCCAAATAAAACGCTTTGGTGGAGGCGGCGAGATGATCCAAAGAGATAATGAGG 301

QY 799 CACAGTTTCTCTCTGAGAGTAAACTGGCAAGATGTATATGATAAAAGCTTTGACTCTCT 858
DB 302 CACAGTTTCTTCTTCTGGAGTAAACTGGCAGGACGCTATATGACAAAGAGCTTTGACTCTCT 361

QY 859 TTTAAACCTCAAGTAACATCTGAGACAGATACTAGATATTTTGTAGAGAAATTTTACAGCT 918
DB 362 TTTAAGCTCAAGTAACATCTGAGACAGATGATGAGACAGACAGATATTTTCGATGAAGATTTTACAGCT 421

QY 919 CAGACTATTACAATAAACACCCACCTGAAATAATAT 951
DB 422 CAGACTATTACAATAAACACCCACCTGAAAGTGT 454

; SEQUENCE 4033, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
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Matches 516; Conservative 0; Mismatches 406; Indels 6; Gaps 2;
Qy 20 GAAAGACAATCAATGATTTTACACTATTGAACTACTAGGTAAAGGCACATTTTGGGAAG 79
Db 1164 GGATGAACACTACCGAATTTTAACTTCCCTAAATGGTGCTGGGGAAGGACGCTTTTGGCAAGG 1223
Qy 80 TTATTTTGGTTTCGAGAGAAGCAAGTGGAAATATCTATGCTATGAAGATCTGAAGAAG 139
Db 1224 TCATGCTTTCAGAACGAAAGGCACAGATGAGCTCTATGCTGTAAGATCTTGAAGAAG 1293
Qy 140 AAGTCATATTGCAAGAGTGAAGTGGCACACACTCTAACTGAAGAGCAGAGTATTAAAGA 199
Db 1284 ACGTTGTGATCCAAGATGACGTGGAGTGCATATGTTGAGAGAGCGGCTGTGGCCC 1343
Qy 200 ACATCT--AGACATCCCTTTTAAACATCTTGAATATTCCTCCAGACAAAGACGTT 256
Db 1344 TGCTGGGAAGCGCCCTTCTGACCCAGCTCCACTCTGCTTCCAGACCAATGAGCCGCC 1403
Qy 257 TGTGTTTGTGATGGAATATGTTAAATGGGGCGAGCTGTTTTTCCATTTTGTGAGAGAGC 316
Db 1404 TGTACTTTGTGATGAGTACGTGAATGGGGCGACCTCATGTATCATCATCCAGCAAGTCG 1463
Qy 317 GGGTGTCTCTGAGAACCGACACAGTTTCTATGTGTGAGAAATTTGTCTGCTCCCTGGACT 376
Db 1464 GCCGGTTCAAGGAGCCCATCTGTATTTTACGCTGCAGAAATTTGCCATCGTCTGTCT 1523
Qy 377 ATCTACATTCGGAAAGATTGTGACGTGATCTCAAGTTGGAGAAATCTAATGCTGGACA 436
Db 1524 TCTTACAGATGAAGGCATCAATTTACCGTGACCTTAAACCTTGACAAAGTATGCTCGATT 1593
Qy 437 AAGATGGCCACATAAAATTTACAGATTTTGGACTTTGCAAGAGAGGGATCACAGATGCAG 496
Db 1584 CTGAGGGACACATCAAGATTGCCGATTTTGGCATGTGTAGGAAACATCTGGGATGGG 1643
Qy 497 CCACATGAAGACATTTCTGGGACATCCAGAAATCTGGGACACAGAGGTGTGAAGATA 556
Db 1644 TGCAACCAAGACATTTCTGGGACATCCAGACTACATCGCCCCCGAGATAATTTGCTTATC 1703
Qy 557 ATGACTATGGCGAGCAGTACAGTGTGGGGCCTAGGGGTTGTCATGTATGAAATGATGT 616
Db 1704 AGCCCTATGGGAAGTCCGTGGAATTTGGGCAATTTGGAGTCCCTGCTGTATGAAATGTGG 1763
Qy 617 GTGGAGGTTACCTTTCTACAAACAGGACCATGAGAACTTTTGAATTTAATTTAATGG 676
Db 1764 CTGGGAGGACACCTTTTGAAGGGAGGATGAAGATGAATCTTCCATCCATATGGAAC 1823
Qy 677 AAGACATTAATTTCTCGAACAATCTCTTTCAGATGCAAAATCAATGCTTTTCAGGGCTCT 736
Db 1824 ACAACGTAGCCTATCCCAAGTCTATGTCCAAAGAAAGCTGTGGCCATCTGCAAAAGGGCTGA 1883
Qy 737 TGATAAAGGATCCAAATAAACCGCTTGGTGAGGACCCAGATGATGCAAAAGAAATTTATGA 796
Db 1884 TGACCAAAACCCAGGCAAGCTCTGGGTTGTGGACCTTGAAGGCGAAGCGTATATCAAG 1943
Qy 797 GACACAGTTCTTCTCTGGAATAAATGGCAAGATGTATATGATAAAAGCTTTGACCTC 856
Db 1944 AGCATGCAATTTTCGGGTATATTGATTGGGAGAACTTGAACGCCAAGAGATCCAGCCCC 2003
Qy 857 CTTTAAACCTCAAGTAAACATCTGAGACAGATATCTAGATATTTTGTATGAAGAAATTTACAG 916
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Db 2061 GCCATCCACAGTCTTAACACCTCCCGA 2088
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RESULT 12

US-11-136-527-2878  
; Sequence 2878, Application US/11136527  
; Publication No. US20050287570A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth

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; APPLICANT: Mounts, William M  
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes  
; FILE REFERENCE: 031896-041000 (AM101086)  
; CURRENT APPLICATION NUMBER: US/11/136,527  
; CURRENT FILING DATE: 2005-05-25  
; PRIOR APPLICATION NUMBER: US 60/574,294  
; PRIOR FILING DATE: 2005-05-26  
; NUMBER OF SEQ ID NOS: 362830  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 2878  
; LENGTH: 2615  
; TYPE: DNA  
; ORGANISM: Rattus norvegicus  
US-11-136-527-2878
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Query Match 24.28; Score 236.4; DB 11; Length 2615;  
Best Local Similarity 55.6%; Pred. No. 2.2e-55;  
Matches 497; Conservative 0; Mismatches 391; Indels 6; Gaps 2;  
Qy 28 ATGAATGATTTTGACTATTGAAACTACTAGGTAAAGGCACATTTTGGGAAAGTTATTTTG 87  
Db 1082 ATCGACAACCTTTGAGTTTCATCCGGGTGTTGGGNAAGGGAGCTTCGGGNAAGTGTATGCTC 1141  
Qy 88 GTTCGAGAGAAGCAAGTGGAAAATACTATGCTATGAAGATTCTGAAGAAGAAAGTCAATT 147  
Db 1142 GCCAGATAAAGGAGACAGGAGAGCTGTACGCTGTGAAGGTGCTGAAAGAGGACGTCAATC 1201  
Qy 148 ATTGCAAGAGATGAAGTGGCACACACACTCTAACTG--AAAGCAGAGATTATTAAGAACACT 204  
Db 1202 CTCAGGATGACCATGTGGAATGCCATGACTGAGAAGAGGATCCCTCTCTTGGCCCGC 1261  
Qy 205 AGACATCCCTTTTAAACATCCTTGMATAATTCCTTCCAGACAAAGACCCTTTGTGTTTTT 264  
Db 1262 AACACCCCTTCTCACCCAGCTTCTCTGCTGCTTTTCAGACTCTCTGACCGTCTGTTCTT 1321  
Qy 265 GTGATGGAATATGTTAAATGGGGCGAGCTGTTTTTCCATTTTGTGAGAGAGCGGTTGTC 324  
Db 1322 GTCATGAGTTTGTGAACGGAGGTGACCTGATGTTCCACATCCAAAAGTCCAGGCGTTTC 1381  
Qy 325 TCTGAGAGACCGCACACGTTTTCTATGTTGCGAGAAATTTGCTCTGCTTGGACTATCTACAT 384  
Db 1382 GATGAAGCCCGAGCTCGTTTTCTACGCTGCGAGAGATCAATTTCTGCACATCATGTTCCCTCCAC 1441  
Qy 385 TCGGGAAGGATTTGTACCGTGATCTCAAGTTGGAGAAATCTAATGCTGGACAAAGATGGC 444  
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Qy 802 AGTTTCTTCTCGAGTAAACTGCGCAAGATGTATATGATAAAAGCTTTGACCTCTCTTTT 861  
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Db 1862 CCTTCTTTAAGGAATCGACTGGTCCAGTTGAACCATGCCAGCTAGAACCGCTTTC 1921  
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RESULT 13  
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; Sequence 2, Application US/11152366  
; Publication No. US20060014184A1  
; GENERAL INFORMATION:  
; APPLICANT: Brys, Reginald  
; APPLICANT: Vandeghinse, Nick  
; APPLICANT: Tomme, Peter H. M.  
; TITLE OF INVENTION: Methods For Identification, And Compounds Useful For The  
; TITLE OF INVENTION: Treatment Of Degenerative & Inflammatory Diseases  
; FILE REFERENCE: P27,880-A USA  
; CURRENT APPLICATION NUMBER: US/11/152,366  
; CURRENT FILING DATE: 2005-06-14  
; PRIOR APPLICATION NUMBER: 60/579,307  
; PRIOR FILING DATE: 2004-06-14  
; NUMBER OF SEQ ID NOS: 295  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 2  
; LENGTH: 5537  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-11-152-366-2  
Query Match 23.5%; Score 229.8; DB 11; Length 5537;  
Best Local Similarity 55.2%; Pred. No. 1.9e-53;  
Matches 494; Conservative 0; Mismatches 392; Indels 9; Gaps 2;  
Qy 29 TGAATGATTTTCACTATTGAACTACTAGGTAAAGGCACCTTTTCGGAAGTATTTTGG 88  
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Qy 89 TTCGAGAGAAGCAAGTGGAAATACTATGCTATGAAGATCTTGAAGAAAGAGTCATTA 148  
Db 1471 CAGAACTCAAGGGCAAGATGAAGTATATGCTGTGAAGTCTTAAAGAGGACGTCATCC 1530  
Qy 149 TTGAAAGATGAAGTGGACACACTCTAACTGAAGACGAGTATT---AAAGAACACTA 205  
Db 1531 TTCAGGATGATGACGTGGACTGCACAATGACAGAGAAGAGGATTTTGGCTCTGGCACGGA 1590  
Qy 206 GACATCCCTTTTAACTCCTTGAATATTCCTCCAGACAAAGACCGTTTGTGTTTG 265  
Db 1591 AACACCGTACCTTACCNACTCTACTGCTGCTTCCAGAACGAGACCGCTCTTTTTCG 1650  
Qy 266 TGATGGAATATGTTAATGGGGCGAGCTGTGTTTCCATTTTTCGAGAGAGCGGGTGTTC 325  
Db 1651 TCATGGAATATGTAATGGTGGAGACCTCATGTTTCAGATTCAGCGCTCCCGAAATTCG 1710  
Qy 326 CTGAGACCGGACACAGTTTCTATGTTGCGAGAAATTTGCTCTGCCCTTGGACTATCTACAT 385  
Db 1711 ACAGACCTCGTTACCGGTTCTATGCTGCAGAGGTCACATCGGCCCTCATGTTCTCCACC 1770  
Qy 386 CCGGAAGATTCGTACCGTGATCTCAAGTTCGAGATCTAATGCTGGACAAAGATGGCC 445  
Db 1771 AGCATGGAGTCATCTACAGGATTTTGAACCTGGACAACTATCCCTTCGTGATGAGAGGTC 1830  
Qy 446 ACATAAAATATACAGATTTTGGACTTTTGAAGAGAGGATTCAGATGAGCCACCATGA 505  
Db 1831 ACTGCAAGCTGGCTGACTTCGGGATGTGCAAGGAGGGATTCGAATGGTGTGACGACCA 1890  
Qy 506 AGACATTCCTGTGGCACTCCAGAAATATCTGGGACCGAGAGTGTAGAGAAATATGACTATG 565  
Db 1891 CCACGCTCTCTGGGACTCTGACTACATAGCTCCTGAGATCTCTGAGAGGATTTGGAGTATG 1950  
Qy 566 GCCGAGCAGTACGTTGGGCGCTAGGGGTTGTCATGTATCAATGATGTCTGGAGGT 625  
Db 1951 GCCCTCCGTGGACTGGTGGGCGCTGCTGATGTACGAGATGATGGCTGGACAGC 2010

Qy 626 TACCTTTCTACACACGAGCCATCGAGAAACTTTTGTGAATTAATTAATGAAGACATTA 685  
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Qy 800 ACAGTTTCTTCTCTGGAGTAAACTGGCGAAGATGTATATGATAAAGAGCTTTGTACCTCTT 859  
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US-11-136-527-1950  
; Sequence 1950, Application US/11136527  
; Publication No. US20050287570A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Mounts, William M  
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes  
; FILE REFERENCE: 031896-041000 (AM101086)  
; CURRENT APPLICATION NUMBER: US/11/136,527  
; CURRENT FILING DATE: 2005-05-25  
; PRIOR APPLICATION NUMBER: US 60/574,294  
; PRIOR FILING DATE: 2005-05-26  
; NUMBER OF SEQ ID NOS: 362830  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 1950  
; LENGTH: 3075  
; TYPE: DNA  
; ORGANISM: Rattus norvegicus  
US-11-136-527-1950  
Query Match 23.5%; Score 229.4; DB 11; Length 3075;  
Best Local Similarity 55.1%; Pred. No. 2e-53;  
Matches 493; Conservative 1; Mismatches 392; Indels 9; Gaps 2;  
Qy 29 TGAATGATTTTGAATTTGAACTACTAGGTAAAGGCACCTTTTCGGAAGTATTTTGG 88  
Db 1407 TGGATGAGTTCACCTTCATCAAGGTGTTAGGCAAAAGGACGCTTTGGCAAGTCACTGCTGG 1466  
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Qy 149 TTGCAAAAGATGAAGTGGCACAACACTCTAACTGAAGACAGAGTATT---AAAGAACACTA 205  
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Qy 206 GACATCCCTTTTAACTATCTTGAATATTCCTCCAGACAAAGACCGTTTGTGTTTG 265  
Db 1587 AACACCTTTATCTAACCCCACTCTATGCTGCTTCCAGACCAAGGACCGCTCTCTTCTCG 1646  
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Qy 506 AGACATTTCTGGGCACCTCCAGAAATATCTGGCACAGAGGTGTTAGAAAGATAATGACTATG 565  
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Qy 626 TACCTTTCTACAACAGCAGCAGCATGAGAAACTTTTTTGAATTAATTAATGAAGACATTA 685  
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US-10-955-054A-34  
; Sequence 34, Application US/10955054A  
; Publication No. US2005026420A1  
; GENERAL INFORMATION:  
; APPLICANT: PUSZTAI, LAJOS  
; APPLICANT: SYMANS, W. FRASER  
; APPLICANT: HESS, KENNETH R.  
; APPLICANT: AYERS, MARK  
; APPLICANT: STEC, JAMES  
; TITLE OF INVENTION: MULTIGENE PREDICTORS OF RESPONSE TO CHEMOTHERAPY  
; FILE REFERENCE: UTXC:880US  
; CURRENT APPLICATION NUMBER: US/10/955,054A  
; CURRENT FILING DATE: 2004-09-30  
; NUMBER OF SEQ ID NOS: 195  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 34  
; LENGTH: 2146  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-955-054A-34

Query Match 23.1%; Score 226.4; DB 7; Length 2146;  
Best Local Similarity 55.1%; Pred. No. 1.2e-52;  
Matches 487; Conservative 0; Mismatches 391; Indels 6; Gaps 2;  
Qy 34 GATTTTGACTATTTTGAAGTAAAGGCACTTTTGGGAAAGTTATTTGGTTTGA 93  
Db 499 GACTTCGACTTCCTCAAGTCATCGGCNAGGGAAGTACGGGAAGGTCCTACTGGCCCAAG 558  
Qy 94 GAGAAGCAAGTGGAATAATCTATGCTATGAAGATCTCGAAGAAAGATCATTTATGCA 153  
Db 559 CGCAAGTCTGATGGGGGTTCTATGCAAGTGAAGGTAATACAGAAAAAGTCCATCTTAAAG 618  
Qy 154 AAGCATGAGTGGCAGACACTCTAACTGAAAGCAGATATTA---AAGACACTAGACAT 210  
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Qy 211 CCCTTTTAAATCCTTTGAAATATTCCTCCAGACAAAAGACCCGTTTGTGTTTGTGATG 270  
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Qy 271 GAATATGTTAATGGGGCGAGCTGTTTTCATTTTGTGAGAGAGCGGGTGTCTCTGAG 330  
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GenCore version 5.1.7  
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OM nucleic - nucleic search, using sw model

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Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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10: /cgn2\_6/ptodata/1/pubpna/US11\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	978	100.0	2811	8	US-10-753-267-107
3	949.8	97.1	1570	3	US-09-526-043-1
4	949.8	97.1	1570	6	US-10-394-568-1
5	949.8	97.1	1570	10	US-11-063-691-1
6	949.8	97.1	1703	9	US-10-887-553A-692
7	689	70.4	2410	3	US-09-771-161A-66
8	527	53.9	1722	7	US-10-323-281-412
9	527	53.9	1741	6	US-10-324-985A-2
10	527	53.9	1741	8	US-10-735-461-21
11	527	53.9	3010	9	US-10-895-225A-57
12	525	53.7	1140	6	US-10-324-985A-5
13	525	53.7	1443	10	US-11-166-990-66
14	525	53.7	2626	7	US-10-324-985A-1
15	525	53.7	2626	7	US-10-713-678-5
16	525	53.7	2626	8	US-10-735-461-20
17	525	53.7	2626	9	US-10-895-225A-56
18	517.4	52.9	2562	7	US-10-322-281-415
19	515.8	52.7	1599	6	US-10-324-985A-3
20	515.8	52.7	1599	7	US-10-641-643-1004
21	515.8	52.7	1715	6	US-10-007-926A-254
22	515.8	52.7	1715	8	US-10-735-461-23
23	512.2	52.4	2729	9	US-10-895-225A-36

24	512.2	52.4	2978	3	US-09-955-999-43	Sequence 43, Appl
25	510.6	52.2	2181	5	US-10-072-036-70	Sequence 70, Appl
26	510.6	52.2	2184	5	US-10-072-036-138	Sequence 138, App
27	510.6	52.2	2610	3	US-09-970-000-3	Sequence 3, Appl1
28	510.6	52.2	2610	6	US-10-388-263-329	Sequence 329, App
29	510.6	52.2	2610	7	US-10-641-643-1206	Sequence 1206, Ap
30	510.6	52.2	2610	7	US-10-713-678-1	Sequence 1, Appl1
31	510.6	52.2	2610	8	US-10-735-461-22	Sequence 22, Appl
32	510.6	52.2	2610	9	US-10-823-433-3	Sequence 3, Appl1
33	510.6	52.2	2610	9	US-10-956-157-1382	Sequence 1382, Ap
34	510.6	52.2	2707	9	US-10-956-157-4334	Sequence 4334, Ap
35	499.6	51.1	1854	5	US-10-198-846-9984	Sequence 9984, Ap
36	493	50.4	1254	7	US-10-713-678-3	Sequence 3, Appl1
37	430.8	44.0	2375	10	US-11-097-143-25901	Sequence 25901, A
38	430.8	44.0	2425	10	US-11-097-143-40607	Sequence 40607, A
39	430.8	44.0	3712	8	US-10-473-939-7	Sequence 7, Appl1
40	429.2	43.9	550	10	US-11-060-756-3130	Sequence 3130, Ap
41	429.2	43.9	550	10	US-11-060-756-3131	Sequence 3131, Ap
42	429.2	43.9	550	10	US-11-060-756-7402	Sequence 7402, Ap
43	429.2	43.9	550	10	US-11-060-756-7403	Sequence 7403, Ap
44	410.6	42.0	2583	9	US-10-450-763-20291	Sequence 20291, A
45	383.8	39.2	387	6	US-10-168-771-2	Sequence 2, Appl1

ALIGNMENTS

RESULT 1  
US-10-324-985A-4  
; Sequence 4, Application US/10324985A  
; Publication No. US20030144204A1  
; GENERAL INFORMATION:  
; APPLICANT: Spencer, David  
; TITLE OF INVENTION: Akt-based Inducible Survival Switch for Gene Therapy  
; FILE REFERENCE: P02248US/10106761  
; CURRENT APPLICATION NUMBER: US/10/324,985A  
; CURRENT FILING DATE: 2002-12-19  
; PRIOR APPLICATION NUMBER: US 60/342,155  
; PRIOR FILING DATE: 2001-12-19  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 4  
; LENGTH: 2811  
; TYPE: DNA  
; ORGANISM: human  
US-10-324-985A-4

Query Match	100.0%	Score	978	DB	6	Length	2811
Best Local Similarity	100.0%	Pred. No.	7.6e-253	Mismatches	0	Indels	0
Matches	978	Conservative	0	0	0	Gaps	0
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Db	406	TCTCAACCCATCATATAAAGAAAGACAATGAATGATTTTGACTATTTTGAACTACTAGT	465				
Qy	61	AAAGCACTTTGGGAAAGTTATTTTGGTTCAGAGAGGCAAGTGGGAAATTAATCTATGCT	120				
Db	466	AAAGCACTTTGGGAAAGTTATTTTGGTTCAGAGAGGCAAGTGGGAAATTAATCTATGCT	525				
Qy	121	ATGAAGATTCGAGAGAGAGTCAATTTTCAAGAGGATGAAGTGGGCAACACTCTAACT	180				
Db	526	ATGAAGATTCGAGAGAGAGTCAATTTTCAAGAGGATGAAGTGGGCAACACTCTAACT	585				
Qy	181	GAAAGCAGAGTATTAAAGAACACATAGACATCCCTTTTAAACATCCCTTGAATATTCCTTC	240				
Db	586	GAAAGCAGAGTATTAAAGAACACATAGACATCCCTTTTAAACATCCCTTGAATATTCCTTC	645				
Qy	241	CAGACAAAAGCCGTTTGTGTTGTTGTAATGTAATGTTGTTGTTGTTGTTGTTGTTGTTT	300				
Db	646	CAGACAAAAGCCGTTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTT	705				
Qy	301	CATTTGTCGAGAGCGGTTCTCTCAGGACCCGACACGTTTCTATGTCGAGAAATTT	360				

Db 706 CATTGTGCGAGAGCGGGTGTCTCTGAGGACCGCACACAGTTTCTATGGTGCAGAAATT 765  
Qy 361 GTCTCTGCTTGGACTACTACATTCGGAAGAGTTGTGTACCGTGATCTCAAGTTGGAG 420  
Db 766 GTCTCTGCTTGGACTACTACATTCGGAAGAGTTGTGTACCGTGATCTCAAGTTGGAG 825  
Qy 421 AATCTAATGCTGGACAAAGATGGCCACATAAAATACAGATTTTGGACTTTTGCAGAA 480  
Db 826 AATCTAATGCTGGACAAAGATGGCCACATAAAATACAGATTTTGGACTTTTGCAGAA 885  
Qy 481 GGGATCACAGATGAGCCACATGAAGACATCTGTGGCACTCAGAAATATCTGGCACCA 540  
Db 886 GGGATCACAGATGAGCCACATGAAGACATCTGTGGCACTCAGAAATATCTGGCACCA 945  
Qy 541 GAGGTGTTAGAAATATGACTATGGCGAGCAGTAGACTGTGGGCGCTAGGGGTTGTC 600  
Db 946 GAGGTGTTAGAAATATGACTATGGCGAGCAGTAGACTGTGGGCGCTAGGGGTTGTC 1005  
Qy 601 ATGTATGAATGATGTGTGGAGGTTACCTTTCTACAAACGAGGACCATGAGAACTTTTT 660  
Db 1006 ATGTATGAATGATGTGTGGAGGTTACCTTTCTACAAACGAGGACCATGAGAACTTTTT 1065  
Qy 661 GAATTAATATTAATGGAAGACATTAATTTCTCTGCAACACTCTCTCAGATGCAAAATCA 720  
Db 1066 GAATTAATATTAATGGAAGACATTAATTTCTCTGCAACACTCTCTCAGATGCAAAATCA 1125  
Qy 721 TTGCTTTGAGGCTCTTGATAAGAGATCCAAATAAACGCCCTTGTGGAGGACCAAGATGAT 780  
Db 1126 TTGCTTTGAGGCTCTTGATAAGAGATCCAAATAAACGCCCTTGTGGAGGACCAAGATGAT 1185  
Qy 781 GCAAAAGAAATATGAGACACAGTTTCTCTCTGAGGTAACTGGCAAGATGTATATGAT 840  
Db 1186 GCAAAAGAAATATGAGACACAGTTTCTCTCTGAGGTAACTGGCAAGATGTATATGAT 1245  
Qy 841 AAAAGCTTGTACCTCTTTTAAACCTCAAGTAAATCTGAGACAGATACAGATATTTT 900  
Db 1246 AAAAGCTTGTACCTCTTTTAAACCTCAAGTAAATCTGAGACAGATACAGATATTTT 1305  
Qy 901 GATGAAGATTTACAGCTCAGACTATTACATAACACACCTGAAATAATATGATGAGAT 960  
Db 1306 GATGAAGATTTACAGCTCAGACTATTACATAACACACCTGAAATAATATGATGAGAT 1365  
Qy 961 GGTATGGACTGCATGGAC 978  
Db 1366 GGTATGGACTGCATGGAC 1383

RESULT 2  
US-10-753-267-107  
; Sequence 107, Application US/10753267  
; Publication No. US20050037946A1  
; GENERAL INFORMATION:  
; APPLICANT: Millennium Pharmaceuticals, Inc.  
; APPLICANT: Stagliano, Nancy E.  
; APPLICANT: Healy, Aileen  
; APPLICANT: Acton, Susan L.  
; APPLICANT: Galvin, Katherine M.  
; APPLICANT: Donoghue, Mary A.  
; APPLICANT: Rodriguez-Way, Amelie  
; APPLICANT: Tomlinson, James E.  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING  
; TITLE OF INVENTION: CARDIOVASCULAR DISEASE USING 1722, 10280, 59917, 85553,  
; TITLE OF INVENTION: 10653, 9235, 21668, 17794, 2210, 6169, 10102, 21061, 17662,  
; TITLE OF INVENTION: 1468, 12282, 6350, 9035, 1820, 23652, 7301, 8925, 8701,  
; TITLE OF INVENTION: 3533, 9462, 9123, 12788, 17729, 65552, 1261, 21476, 33770,  
; TITLE OF INVENTION: 9380, 2569654, 33556, 53656, 44143, 32612, 10671, 261,  
; TITLE OF INVENTION: 44570, 41922, 2552, 2417, 19319, 43969, 8921, 8993, 955,  
; TITLE OF INVENTION: 32345, 966, 1920, 17318, 1510, 14180, 26005, 554, 16408,  
; TITLE OF INVENTION: 42028, 112091, 13886, 13942, 1673, 54946 OR 2419  
; FILE REFERENCE: MPI03-003P18NOWNIM  
; CURRENT APPLICATION NUMBER: US/10753,267  
; CURRENT FILING DATE: 2004-01-08  
; PRIOR APPLICATION NUMBER: US 60/439,683

; PRIOR FILING DATE: 2003-01-13  
; PRIOR APPLICATION NUMBER: US 60/445,216  
; PRIOR FILING DATE: 2003-02-05  
; PRIOR APPLICATION NUMBER: US 60/448,036  
; PRIOR FILING DATE: 2003-02-18  
; PRIOR APPLICATION NUMBER: US 60/454,189  
; PRIOR FILING DATE: 2003-03-12  
; PRIOR APPLICATION NUMBER: US 60/457,541  
; PRIOR FILING DATE: 2003-03-25  
; PRIOR APPLICATION NUMBER: US 60/466,411  
; PRIOR FILING DATE: 2003-04-29  
; PRIOR APPLICATION NUMBER: US 60/469,041  
; PRIOR FILING DATE: 2003-05-08  
; PRIOR APPLICATION NUMBER: US 60/477,414  
; PRIOR FILING DATE: 2003-06-10  
; PRIOR APPLICATION NUMBER: US 60/478,560  
; PRIOR FILING DATE: 2003-06-13  
; PRIOR APPLICATION NUMBER: US 60/489,772  
; PRIOR FILING DATE: 2003-07-24  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 130  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 107  
; LENGTH: 2811  
; TYPE: DNA  
; ORGANISM: Homo Sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)...(1440)  
; US-10-753-267-107

Query Match 100.0%; Score 978; DB 8; Length 2811;  
Best Local Similarity 100.0%; Pred. No. 7 5e-253;  
Matches 978; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 TCTACAACCCATCATAAAAGAAAGACAAATGAATGATTTTGCACATATTTGAAACTACTAGGT 60  
Db 406 TCTACAACCCATCATAAAAGAAAGACAAATGAATGATTTTGCACATATTTGAAACTACTAGGT 465  
Qy 61 AAAGGCACATTTTGGGAAAGTTATTTTGGTTCGAGAGAGGCAAGTGGAAATATCTATGCT 120  
Db 466 AAAGGCACATTTTGGGAAAGTTATTTTGGTTCGAGAGAGGCAAGTGGAAATATCTATGCT 525  
Qy 121 ATGAAGATTTCTGAAGAAAGAAAGTCATTATTGCAAGGATGAAGTGGCACACACTCTAACT 180  
Db 526 ATGAAGATTTCTGAAGAAAGAAAGTCATTATTGCAAGGATGAAGTGGCACACACTCTAACT 585  
Qy 181 GAAAGCAGAGTATTAAAGAAACACATAGACATCCCTTTTAAACATCCTTTGAAATATCTCTTC 240  
Db 586 GAAAGCAGAGTATTAAAGAAACACATAGACATCCCTTTTAAACATCCTTTGAAATATCTCTTC 645  
Qy 241 CAGACAAAGACCGTTTGTGTTTGTGATGGAATATGTTAATGGGGCGAGCTGTTTTTC 300  
Db 646 CAGACAAAGACCGTTTGTGTTTGTGATGGAATATGTTAATGGGGCGAGCTGTTTTTC 705  
Qy 301 CATTGTGCGAGAGCGGGTGTCTCTGAGAGCGGCACACAGCTTTCTATGTGCGAGAAATT 360  
Db 706 CATTGTGCGAGAGCGGGTGTCTCTGAGAGCGGCACACAGCTTTCTATGTGCGAGAAATT 765  
Qy 361 GTCTCTGCTTGGACTATCTACATTCGGAAGAGATGTGTACCGTGATCTCAAGTTGGAG 420  
Db 766 GTCTCTGCTTGGACTATCTACATTCGGAAGAGATGTGTGTACCGTGATCTCAAGTTGGAG 825  
Qy 421 AATCTAATGCTGCAAGAGATGGCCACATAAAATATACAGATTTTGGACTTTTGCAGAA 480  
Db 826 AATCTAATGCTGCAAGAGATGGCCACATAAAATATACAGATTTTGGACTTTTGCAGAA 885  
Qy 481 GGGATCACAGATGAGCCACCATGAAGACATCTGTGGCACTCAGAAATATCTGGCACCA 540  
Db 886 GGGATCACAGATGAGCCACCATGAAGACATCTGTGGCACTCAGAAATATCTGGCACCA 945  
Qy 541 GAGGTGTTAGAAATATGACTATGCGCGAGCAGTAGACTGTGGGCGCTAGGGGTTGTC 600

Db 946 GAGGTCTTAGAAGATAATGACTATATGGCCGAGCAGTAGACTGTGTGGGCGCTAGGGGTTGTC 1005  
QY 601 ATGTATGAAATGATGTGTGGAGGTTA CTTTCTCAACCCAGGACCATGAGAAA CTTTTT 660  
Db 1006 ATGTATGAAATGATGTGTGGAGGTTA CTTTCTCAACCCAGGACCATGAGAAA CTTTTT 1065  
QY 661 GAATTAATTAATTAATGGAACACATTAATTTTCTCCGAAACACTCTCTTCAGATGCAAAATCA 720  
Db 1066 GAATTAATTAATTAATGGAACACATTAATTTTCTCCGAAACACTCTCTTCAGATGCAAAATCA 1125  
QY 721 TTGCTTTTCAAGGCTCTTGTATAAAGGATCCAAATAAAGCGCTTTGGTGGAGGACCATGAT 780  
Db 1126 TTGCTTTTCAAGGCTCTTGTATAAAGGATCCAAATAAAGCGCTTTGGTGGAGGACCATGAT 1185  
QY 781 GCAAAAGAAATTAATGAGACACAGTTTCTTCTCTGAGATGAATCTGGCAAGATGATATGAT 840  
Db 1186 GCAAAAGAAATTAATGAGACACAGTTTCTTCTCTGAGATGAATCTGGCAAGATGATATGAT 1245  
QY 841 AAAAGCTGTACCTCTTTTAAACCTCAAGTAAACATCTGAGACAGATAGATATTTT 900  
Db 1246 AAAAGCTGTACCTCTTTTAAACCTCAAGTAAACATCTGAGACAGATAGATATTTT 1305  
QY 901 GATGAAGAAATTAATGAGCTCAGACTATTACAATAACACCACTGAAATAATATGATGAGAT 960  
Db 1306 GATGAAGAAATTAATGAGCTCAGACTATTACAATAACACCACTGAAATAATATGATGAGAT 1365

RESULT 3

US-09-526-043-1  
; Sequence 1, Application US/09526043  
; Publication No. US20030100049A1  
; GENERAL INFORMATION:  
; APPLICANT: Guo, Kun  
; APPLICANT: Pagnoni, Marco  
; APPLICANT: Clark, Kenneth  
; APPLICANT: Ivashchenko, Yuri  
; TITLE OF INVENTION: AKT NUCLEIC ACIDS, POLYPEPTIDES, AND USES THEREOF  
; FILE REFERENCE: A3278A-US  
; CURRENT FILING DATE: 2000-03-14  
; EARLIER FILING DATE: 60/125,108  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 1570  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (126)..(1523)  
US-09-526-043-1

Query Match 97.1%; Score 949.8; DB 3; Length 1570;  
Best Local Similarity 99.8%; Pred. No. 2.3e-245;  
Matches 951; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 TCTACAACCCATCATAAAAGAGCAATGAATGATTTTGGTTCAGAGAAGCGAAGTGGAAAACTACTAGT 60  
Db 531 TCTACAACCCATCATAAAAGAGCAATGAATGATTTTGGTTCAGAGAAGCGAAGTGGAAAACTACTAGT 590  
QY 61 AAAGGCACTTTGGGAAAGTATTTTGGTTCAGAGAAGCGAAGTGGAAAACTACTAGT 120  
Db 591 AAAGGCACTTTGGGAAAGTATTTTGGTTCAGAGAAGCGAAGTGGAAAACTACTAGT 650  
QY 121 ATGAAGATTCTGAAGAAAGAGTCATTATTGCAAAAGGATGAAGTGGCAACACTCTAACT 180  
Db 651 ATGAAGATTCTGAAGAAAGAGTCATTATTGCAAAAGGATGAAGTGGCAACACTCTAACT 710

QY 191 GAAAGCAGAGTATTAAAGAACACTAGACATCCCTTTTAAACATCCTTGAATAATTCCCTTC 240  
Db 711 GAAAGCAGAGTATTAAAGAACACTAGACATCCCTTTTAAACATCCTTGAATAATTCCCTTC 770  
QY 241 CAGACAAAAGACCGTTTGTGTGTGATGGAATATGTTAATGGGGGCGAGCTGTTTTTC 300  
Db 771 CAGACAAAAGACCGTTTGTGTGTGATGGAATATGTTAATGGGGGCGAGCTGTTTTTC 830  
QY 301 CATTTGTCGAGAGACGGGTGTTCTCTGAGCACCGCACACAGTTTCTATGTGTGTCGAGAAAT 360  
Db 831 CATTTGTCGAGAGACGGGTGTTCTCTGAGCACCGCACACAGTTTCTATGTGTGTCGAGAAAT 890  
QY 361 GTCCTGCTTGGACTATCTACATTCGCGAAAGATGTTGTACCGTGATCTCAAGTTGGAG 420  
Db 891 GTCCTGCTTGGACTATCTACATTCGCGAAAGATGTTGTACCGTGATCTCAAGTTGGAG 950  
QY 421 AATCTAATGCTGGACAAAGATGGCCACATAAAATTTACAGATTTTGGACTTTTGCAGAA 480  
Db 951 AATCTAATGCTGGACAAAGATGGCCACATAAAATTTACAGATTTTGGACTTTTGCAGAA 1010  
QY 481 GGGATCACAGATGCGACGCCACCATGAAGACATTTCTGTGGCACTCCAGAAATATCTGGACCA 540  
Db 1011 GGGATCACAGATGCGACGCCACCATGAAGACATTTCTGTGGCACTCCAGAAATATCTGGACCA 1070  
QY 541 GAGGTGTTAGAAGATAATGACTATGCGCCGAGCAGTAGACTGGTGGGGCTTAGGGGTTGTC 600  
Db 1071 GAGGTGTTAGAAGATAATGACTATGCGCCGAGCAGTAGACTGGTGGGGCTTAGGGGTTGTC 1130  
QY 601 ATGTATGAAATGATGTGTGGAGGTTACCTTTCTACAACCCAGGACCATGAGAAACCTTTTT 660  
Db 1131 ATGTATGAAATGATGTGTGGAGGTTACCTTTCTACAACCCAGGACCATGAGAAACCTTTTT 1190  
QY 661 GAATTAATTAATTAATGGAAGACATTTAAATTTCTCGAACA CTTCTTTCAGATGCAAAATCA 720  
Db 1191 GAATTAATTAATTAATGGAAGACATTTAAATTTCTCGAACA CTTCTTTCAGATGCAAAATCA 1250  
QY 721 TTGCTTTCAGGCTCTTGATAAAGATCCAAATAAAGCGCTTGGTGGAGGACCATGAT 780  
Db 1251 TTGCTTTCAGGCTCTTGATAAAGATCCAAATAAAGCGCTTGGTGGAGGACCATGAT 1310  
QY 781 GCAAAAGAAATTTATGAGACACAGATTTTCTTCTGGAGTAAACCTGGCAAGATGATATGAT 840  
Db 1311 GCAAAAGAAATTTATGAGACACAGATTTTCTTCTGGAGTAAACCTGGCAAGATGATATGAT 1370  
QY 841 AAAAGCTTGTACCTCTCTTTTAAACCTCAAGTAAACATCTGAGACAGATAGATATTTT 900  
Db 1371 AAAAGCTTGTACCTCTCTTTTAAACCTCAAGTAAACATCTGAGACAGATAGATATTTT 1430  
QY 901 GATGAAGAAATTTACAGCTCAGACTATTACAATAACACCACTGAAAAATATGA 953  
Db 1431 GATGAAGAAATTTACAGCTCAGACTATTACAATAACACCACTGAAAAATATGA 1483

RESULT 4

US-10-394-568-1  
; Sequence 1, Application US/10394568  
; Publication No. US20040002136A1  
; GENERAL INFORMATION:  
; APPLICANT: GUO, KUN  
; APPLICANT: IVASHCHENKO, YURI  
; APPLICANT: CLARK, KENNETH L.  
; TITLE OF INVENTION: INDUCTION OF VASCULAR ENDOTHELIAL GROWTH FACTOR (VEGF)  
; FILE REFERENCE: A3399WO  
; CURRENT FILING DATE: 2003-03-21  
; PRIOR FILING DATE: 2000-06-01  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 1570  
; TYPE: DNA

; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (126)..(1523)  
US-10-394-568-1

Query Match 97.1%; Score 949.8; DB 6; Length 1570;  
Best Local Similarity 99.8%; Pred. No. 2.3e-245;  
Matches 951; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 1 TCTACACCCATCATAAAGAAAGACATGAATGATTTTGACTATTGTGAACTACTAGGT 60
DB 531 TCTACACCCATCATAAAGAAAGACATGAATGATTTTGACTATTGTGAACTACTAGGT 590
QY 61 AAAGGCATTTTGGGAAAGTTATTTTGGTTCGAGAGAGGCAAGTGGAAATATCTATGCT 120
DB 591 AAAGGCATTTTGGGAAAGTTATTTTGGTTCGAGAGAGGCAAGTGGAAATATCTATGCT 650
QY 121 ATGAAGATTTCTGAAGAAAGAGTCAATATTTCGAAAGGATGAAGTGGCACACACTCTAACT 180
DB 651 ATGAAGATTTCTGAAGAAAGAGTCAATATTTCGAAAGGATGAAGTGGCACACACTCTAACT 710
QY 181 GAAAGCAGAGTATTAAAGAACACATAGACATCCCTTTTAAACATCTCTGAAATATTCCTTC 240
DB 711 GAAAGCAGAGTATTAAAGAACACATAGACATCCCTTTTAAACATCTCTGAAATATTCCTTC 770
QY 241 CAGACAAAGACCGTTTGTGTTTGTGATGGAATATGTTAATGGGCGAGCTGTTTTTC 300
DB 771 CAGACAAAGACCGTTTGTGTTTGTGATGGAATATGTTAATGGGCGAGCTGTTTTTC 830
QY 301 CATTTGTGAGAGCGGGTGTCTCTGAGACCGCACACAGTTTCTATGTCGAGAAATT 360
DB 831 CATTTGTGAGAGCGGGTGTCTCTGAGACCGCACACAGTTTCTATGTCGAGAAATT 890
QY 361 GTCTCTGCTTGGACTATCTACATTCGGAAAGATTGTGTACCGTGATCTCAAGTTGGAG 420
DB 891 GTCTCTGCTTGGACTATCTACATTCGGAAAGATTGTGTACCGTGATCTCAAGTTGGAG 950
QY 421 AATCTAATGCTGGACAAAGATGGCCACATAAAATTTACAGATTTTGGACTTTGCAAGAA 480
DB 951 AATCTAATGCTGGACAAAGATGGCCACATAAAATTTACAGATTTTGGACTTTGCAAGAA 1010
QY 481 GGGATCAAGATGCGACCCACCATGAAGACATTTCTGTGSCACTCCAGAAATATCTGGCACCA 540
DB 1011 GGGATCAAGATGCGACCCACCATGAAGACATTTCTGTGSCACTCCAGAAATATCTGGCACCA 1070
QY 541 GAGGTGTTAGAAATATGACTATGCGGAGCAGTAGACTGGTGGGGCTTAGGGGTTGTC 600
DB 1071 GAGGTGTTAGAAATATGACTATGCGGAGCAGTAGACTGGTGGGGCTTAGGGGTTGTC 1130
QY 601 ATGTATGAAATGATGTGGGAGGTTTACCTTTCTACAAACAGGACCATGAGAAATTTTT 660
DB 1131 ATGTATGAAATGATGTGGGAGGTTTACCTTTCTACAAACAGGACCATGAGAAATTTTT 1190
QY 661 GAATTAATATTAATGGAAGACATTAATTTTCTCGAACACTCTCTTCAGATGCAAAATCA 720
DB 1191 GAATTAATATTAATGGAAGACATTAATTTTCTCGAACACTCTCTTCAGATGCAAAATCA 1250
QY 721 TTGCTTTTCAGGGCTCTTGATAAAGATCAAAATTAAGCCCTTGTGGAGGACGATGAT 780
DB 1251 TTGCTTTTCAGGGCTCTTGATAAAGATCAAAATTAAGCCCTTGTGGAGGACGATGAT 1310
QY 781 GCAAAAGAAATATGAGACACAGTTTCTCTCTGAGTAAACTGGCAGATGTATATGAT 840
DB 1311 GCAAAAGAAATATGAGACACAGTTTCTCTCTGAGTAAACTGGCAGATGTATATGAT 1370
QY 841 AAAAAGCTTGTACCTCTCTTTTAAACCTCAAGTAACATCTGAGACAGATFACTAGATATTTT 900
DB 1371 AAAAAGCTTGTACCTCTCTTTTAAACCTCAAGTAACATCTGAGACAGATFACTAGATATTTT 1430
QY 901 GATGAAGATTTAGAGCTCAGACTATTACAAATACACACCCTGAAATAATGTA 953
DB 1431 GATGAAGATTTAGAGCTCAGACTATTACAAATACACACCCTGAAATAATGTA 1483
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RESULT 5

US-11-063-691-1  
; Sequence 1, Application US/11063691  
; Publication No. US20050142603A1  
; GENERAL INFORMATION:  
; APPLICANT: Guo, Kun  
; APPLICANT: Pagnoni, Marco  
; APPLICANT: Clark, Kenneth  
; APPLICANT: Ivashchenko, Yuri  
; TITLE OF INVENTION: AKT NUCLEIC ACIDS, POLYPEPTIDES, AND USES THEREOF  
; FILE REFERENCE: A3278A-US  
; CURRENT APPLICATION NUMBER: US/11/063,691  
; PRIOR FILING DATE: 2005-02-23  
; PRIOR APPLICATION NUMBER: US/09/526,043  
; PRIOR FILING DATE: 2000-03-14  
; PRIOR APPLICATION NUMBER: 60/125,108  
; PRIOR FILING DATE: 1999-03-19  
; NUMBER OF SEQ ID NOS: 17  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 1570  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (126)..(1523)  
US-11-063-691-1

Query Match 97.1%; Score 949.8; DB 10; Length 1570;  
Best Local Similarity 99.8%; Pred. No. 2.3e-245;  
Matches 951; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 1 TCTACACCCATCATAAAGAAAGACATGAATGATTTTGACTATTGTGAACTACTAGGT 60
DB 531 TCTACACCCATCATAAAGAAAGACATGAATGATTTTGACTATTGTGAACTACTAGGT 590
QY 61 AAAGGCATTTTGGGAAAGTTATTTTGGTTCGAGAGAGGCAAGTGGAAATATCTATGCT 120
DB 591 AAAGGCATTTTGGGAAAGTTATTTTGGTTCGAGAGAGGCAAGTGGAAATATCTATGCT 650
QY 121 ATGAAGATTTCTGAAGAAAGAGTCAATATTTCGAAAGGATGAAGTGGCACACACTCTAACT 180
DB 651 ATGAAGATTTCTGAAGAAAGAGTCAATATTTCGAAAGGATGAAGTGGCACACACTCTAACT 710
QY 181 GAAAGCAGAGTATTAAAGAACACATAGACATCCCTTTTAAACATCTCTGAAATATTCCTTC 240
DB 711 GAAAGCAGAGTATTAAAGAACACATAGACATCCCTTTTAAACATCTCTGAAATATTCCTTC 770
QY 241 CAGACAAAGACCGTTTGTGTTTGTGATGGAATATGTTAATGGGCGAGCTGTTTTTC 300
DB 771 CAGACAAAGACCGTTTGTGTTTGTGATGGAATATGTTAATGGGCGAGCTGTTTTTC 830
QY 301 CATTTGTGAGAGCGGGTGTCTCTGAGACCGCACACAGTTTCTATGTCGAGAAATT 360
DB 831 CATTTGTGAGAGCGGGTGTCTCTGAGACCGCACACAGTTTCTATGTCGAGAAATT 890
QY 361 GTCTCTGCTTGGACTATCTACATTCGGAAAGATTGTGTACCGTGATCTCAAGTTGGAG 420
DB 891 GTCTCTGCTTGGACTATCTACATTCGGAAAGATTGTGTACCGTGATCTCAAGTTGGAG 950
QY 421 AATCTAATGCTGGACAAAGATGGCCACATAAAATTTACAGATTTTGGACTTTGCAAGAA 480
DB 951 AATCTAATGCTGGACAAAGATGGCCACATAAAATTTACAGATTTTGGACTTTGCAAGAA 1010
QY 481 GGGATCAAGATGCGACCCACCATGAAGACATTTCTGTGSCACTCCAGAAATATCTGGCACCA 540
DB 1011 GGGATCAAGATGCGACCCACCATGAAGACATTTCTGTGSCACTCCAGAAATATCTGGCACCA 1070
QY 541 GAGGTGTTAGAAATATGACTATGCGGAGCAGTAGACTGGTGGGGCTTAGGGGTTGTC 600
DB 1071 GAGGTGTTAGAAATATGACTATGCGGAGCAGTAGACTGGTGGGGCTTAGGGGTTGTC 1130
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QY 601 ATGTATGAATGATGCTGGGAGGTACCTTTCTCAACACGAGCAGCATGAGAAACTTTTT 660  
Db 1131 ATGTATGAATGATGCTGGGAGGTACCTTTCTCAACACGAGCAGCATGAGAAACTTTTT 1190  
QY 661 GAAATTAATTAATGGAAGACATTAATTTCTCTCGAACACTCTCTTCAGATGCAAAATCA 720  
Db 1191 GAAATTAATTAATGGAAGACATTAATTTCTCTCGAACACTCTCTTCAGATGCAAAATCA 1250  
QY 721 TTGCTTTTCAGGCTCTTGATAAAGGATCCAAATAAACGCCCTTGGTGGAGGCCAGATGAT 780  
Db 1251 TTGCTTTTCAGGCTCTTGATAAAGGATCCAAATAAACGCCCTTGGTGGAGGCCAGATGAT 1310  
QY 781 GCAAAAGAAATTAATGAGACAGATTTCTCTCTGAGCTAAACTGCGAAGATGTATATGAT 840  
Db 1311 GCAAAAGAAATTAATGAGACAGATTTCTCTCTGAGCTAAACTGCGAAGATGTATATGAT 1370  
QY 841 AAAAAGCTTGTACCTCTCTTTTAAACCTCAAGTAACATCTGAGACAGATAGATATATTT 900  
Db 1371 AAAAAGCTTGTACCTCTCTTTTAAACCTCAAGTAACATCTGAGACAGATAGATATATTT 1430  
QY 901 GATGAAGAAATTAACAGCTCAGACTATTAACAATAACACCACTGAAAAATATGA 953  
Db 1431 GATGAAGAAATTAACAGCTCAGACTATTAACAATAACACCACTGAAAAATATGCA 1483

RESULT 6  
US-10-887-553A-692  
; Sequence 692, Application US/10887553A  
; Publication No. US20050085436A1  
; GENERAL INFORMATION:  
; APPLICANT: Garza, Dan  
; APPLICANT: Li, Hao  
; TITLE OF INVENTION: Method to treat conditions associated  
; with insulin signalling dysregulation  
; FILE REFERENCE: 4-33262  
; CURRENT APPLICATION NUMBER: US/10/887,553A  
; CURRENT FILING DATE: 2004-07-08  
; PRIOR APPLICATION NUMBER: 60/485,883  
; PRIOR FILING DATE: 2003-08-07  
; NUMBER OF SEQ ID NOS: 1208  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 692  
; LENGTH: 1703  
; TYPE: DNA  
; ORGANISM: human  
US-10-887-553A-692

Query Match 97.1%; Score 949.8; DB 9; Length 1703;  
Best Local Similarity 99.8%; Pred. No. 2.4e-245;  
Matches 951; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TCTACAACCCATCATATAAAGAAAGCAATGAATGATTTTGACTATTTGAAACTACTAGGT 60  
Db 487 TCTACAACCCATCATATAAAGAAAGCAATGAATGATTTTGACTATTTGAAACTACTAGGT 546  
QY 61 AAAGGCATTTTGGGAAAGTATTTTGGTTCGAGAGAAGGCAAGTGGAAAAATACTATGCT 120  
Db 547 AAAGGCATTTTGGGAAAGTATTTTGGTTCGAGAGAAGGCAAGTGGAAAAATACTATGCT 606  
QY 121 ATGAAGATCTGAAGAAAGAGTCAATTTGTCGAAAGGATGAAGTGGGCACACACTTAAT 180  
Db 607 ATGAAGATCTGAAGAAAGAGTCAATTTGTCGAAAGGATGAAGTGGGCACACACTTAAT 666  
QY 181 GAAACGAGATTAATAAGAACACTAGACATCCCTTTTAAACATCTTCAAAATATTTCCCTTC 240  
Db 667 GAAACGAGATTAATAAGAACACTAGACATCCCTTTTAAACATCTTCAAAATATTTCCCTTC 726  
QY 241 CAGACAAAAGACCGTTTGTGTTTGTGATGGAATATGTAATGGGGGGGAGCTGTTTTC 300  
Db 727 CAGACAAAAGACCGTTTGTGTTTGTGATGGAATATGTAATGGGGGGGAGCTGTTTTC 786  
QY 301 CATTTGTCGAGAGAGCGGGGTGTTCTCTGAGGACCGCACACGTTTCTATGGTGCAGAAAT 360

Db 787 CATTTGTCGAGAGAGCGGGTGTCTCTGAGGACCGCACACGTTTCTATGGTGCAGAAAT 846  
QY 361 GTCTCTGCTTGGGACTATCTACATTCGGAAGAGATTGTGTACCGGTGATCTCAAGTTGGAG 420  
Db 847 GTCTCTGCTTGGGACTATCTACATTCGGAAGAGATTGTGTACCGGTGATCTCAAGTTGGAG 906  
QY 421 AATCTAATGCTGGGACAAAGATGGCCACATAAAATAATACAGATTTTGGACTTTTGCAGAA 480  
Db 907 AATCTAATGCTGGGACAAAGATGGCCACATAAAATAATACAGATTTTGGACTTTTGCAGAA 966  
QY 481 GGGATCACAGATGAGCCACCATGAAGACATTTCTGTGCACTCCAGAAATATCTGSCACCA 540  
Db 967 GGGATCACAGATGAGCCACCATGAAGACATTTCTGTGCACTCCAGAAATATCTGSCACCA 1026  
QY 541 GAGGTGTTTGAAGATAATGACTATGGCCGAGCAGTAGACTGTGTGGGGCTTAGGGGTGTGC 600  
Db 1027 GAGGTGTTTGAAGATAATGACTATGGCCGAGCAGTAGACTGTGTGGGGCTTAGGGGTGTGC 1086  
QY 601 ATGTATGAATGATGTGTGGGAGGTACCTTTCTACAACGAGGACCATGAGAACTTTT 660  
Db 1087 ATGTATGAATGATGTGTGGGAGGTACCTTTCTACAACGAGGACCATGAGAACTTTT 1146  
QY 661 GAAATTAATTAATGGAAGACATTAATTTCTCGAACACTCTCTTCAGATGCAAAATCA 720  
Db 1147 GAAATTAATTAATGGAAGACATTAATTTCTCGAACACTCTCTTCAGATGCAAAATCA 1206  
QY 721 TTGCTTTTCAGGCTCTTTGATAAAGGATCCAAATAAACGCCCTTGGTGGAGGACCATGAT 780  
Db 1207 TTGCTTTTCAGGCTCTTTGATAAAGGATCCAAATAAACGCCCTTGGTGGAGGACCATGAT 1266  
QY 781 GCAAAAGAAATTAATGAGACACAGATTTTCTCTCGAGTAAACTGGAAGATGTATATGAT 840  
Db 1267 GCAAAAGAAATTAATGAGACACAGATTTTCTCTCGAGTAAACTGGAAGATGTATATGAT 1326  
QY 841 AAAAGCTTGTACCTCTTTTAAACCTCAAGTAACTCTGAGACAGATAGATATTTT 900  
Db 1327 AAAAGCTTGTACCTCTTTTAAACCTCAAGTAACTCTGAGACAGATAGATATTTT 1386  
QY 901 GATGAAGAAATTAACAGCTCAGACTATTAACAATAACACCACTGAAAAATATGA 953  
Db 1387 GATGAAGAAATTAACAGCTCAGACTATTAACAATAACACCACTGAAAAATATGA 1439

RESULT 7  
US-09-771-161A-66  
; Sequence 66, Application US/09771161A  
; Patent No. US20020110811A1  
; GENERAL INFORMATION:  
; APPLICANT: LEVINE, et al.  
; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES  
; FILE REFERENCE: 802620-2005.1  
; CURRENT APPLICATION NUMBER: US/09/771,161A  
; CURRENT FILING DATE: 2001-01-26  
; PRIOR APPLICATION NUMBER: 09/724,676  
; PRIOR FILING DATE: 2000-11-28  
; PRIOR APPLICATION NUMBER: 136776  
; PRIOR FILING DATE: 2000-06-15  
; PRIOR APPLICATION NUMBER: 135619  
; PRIOR FILING DATE: 2000-04-12  
; NUMBER OF SEQ ID NOS: 273  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 66  
; LENGTH: 2410  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-771-161A-66

Query Match 70.4%; Score 689; DB 3; Length 2410;  
Best Local Similarity 100.0%; Pred. No. 7.3e-175;  
Matches 689; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 290 AGCTGTTTTTCCATTTTTCGAGAGAGCGGGTGTCTCTGAGGACCGCACACGTTTCTATG 349



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; PRIOR APPLICATION NUMBER: US 60/342,155
; PRIOR FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 1741
; TYPE: DNA
; ORGANISM: mouse
; US-10-324-985A-2

Query Match          53.9%;   Score 527;   DB 6;   Length 1741;
Best Local Similarity 72.7%;   Pred No. 3.3e-131;
Matches 680;   Conservative 0;   Mismatches 255;   Indels 0;   Gaps 0;

Qy      19  AGAAGACAATGAATGATTTTGACTATTTCGAACTACTAGTAAAGCACCTTTTGGGAAA  78
Db      652  AAAGTGACCATGAATGACTTCGATTATCTCAAACCTCTCGCAAGGCGACCTTCGGCAAG  711

Qy      79  GTTATTTTGGTTCAGAGAGAGCGCAAGTGGAAAAATACATGCTATGAAGATTCCTGAAGAAA  138
Db      712  GTCATTCTGGTTCAGAGAGAGCGCACCTGGCGCGCTATTATGTCATGAAGATCCTCTCGCAAG  771

Qy      139  GAAGTCATTATGCAAGAGGTGAAGTCGGCACACACTCTAACTGAAACGAGAGATTAAAG  198
Db      772  GAGGTCTCATATGCAAGAGGATGAAGTCGCCACACAGTCAAGAGAGCGGGTTCCTCGAG  831

Qy      199  AACACTAGACATCCCTTTTAAACATCCTTGAATAATTTCCTTCCAGACAAAAGACCGTTTG  258
Db      832  AATACCAGGCACCCCTTCCTTACAGCCCTCAAGTATGCCTTCCAGACCCCATGACCGCTA  891

Qy      259  TGTTTTGTGATGGAAATATGTTAAATGCGGGCGAGCTGTTTTTCCATTTGTCGAGAGAGCGG  318
Db      892  TGCCTTGTGATGGAGTATGCCAACGGGGGTGAGCTGTTTTTCCACCTCTCTCGGAGCGCA  951

Qy      319  GTGTTCTCTGAGGACCGCACACGCTTCTATGTTGTCAGAAATATGCTCTGCTTGGACTAT  378
Db      952  GTCTTTCAGGAGGATCGGGCGCGCTTTATATGAGCAGAGATTGTGTGAGTCTCTGGAGTAT  1011

Qy      379  CTACATTTCCGAAAGATTGTGTACCGCTGATCTCAAAGTTGGAGAAATCTAAATGCTCGACAA  438
Db      1012  TTGCACCTCGAGAGATGTGTTGATCCGTGACATCAAGCTGGNAAACCTTATGTTGGACAA  1071

Qy      439  GATGGCCACATAAAAATTTACAGATTTTGGACTTTTGCAAGAGAGGATCAAGATGCGAGCC  498
Db      1072  GATGGCCACATCAAGATCACTGACTTTTGGCTTTGTGCAAGAGGCGCATCAGTGATGGAGCC  1131

Qy      499  ACCATGAAGACATTTCTGTGGCATCTCAGAAATATCTGGGACACAGAGGTGTTAGAAGATAAT  558
Db      1132  ACCATGAAACCTTCTGTGTGTACCCGGAGTACTTGGCGCTGAGGTGCTAGAGAGACAAT  1191

Qy      559  GACTATGCGCGAGCAGTAGACTGTGTGGCGCTAGGGGTGTGTCATGATGAAATCATGTGT  618
Db      1192  GACTATGGCGGAGCAGTGGACTGTGTGGGGCTTGGGTGTGTGTCATGATGAGATGATGTGT  1251

Qy      619  GGGAGGTTACCTTTCTACAAACGAGGACCATGAGAAACCTTTTGGAAATTAATTAATGGAA  678
Db      1252  GGCGCGCTGCCATTTCTAACACGAGCACCAAGCGCGCTCTTTGAGCTCATTTATGAG  1311

Qy      679  GACATTAATTTTCTTCGAACTCTCTTCAGATCGAAAAATCATTTGCTTTTCAAGGCTCTTG  738
Db      1312  GAGATCGGCTTTCGCGCGCACACTCGGGCCAGAGGCCAAGTCCCTGCTGGCTGGAATGCTG  1371

Qy      739  ATAAGGATCCAAATAACGCCCTTGTGTGGAGGACAGATGATGCAAGAAATTAATCAGA  798
Db      1372  AAGAAGGACCCAAAGCAGAGGCTCTGGCGGAGGTCCCGAGTGATGCGAAGGAGGTATCGAG  1431

Qy      799  CACAGTTTCTTCTCTGGAGTAAAATGCGCAAGATGTATATGATGATAAAAAAGCTTTGTACCTCCT  858
Db      1432  CATAGATTCCTCTCAGCATCAAATGCGCAGGACGTTGTACAGAAAAGCTCTCTGCCACCC  1491

Qy      859  TTTAAACCTCAAGTAAACATCTGAGACAGATACTAGATTAATTTTGATGAAGAAATTTACAGCT  918
Db      1492  TTCAAACCTCAGGTCACTTCAGAAAGTGACACAAGGTACTTTGATGACAGAGTTCACGCGC  1551

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Qy	919	CAGACATATTACATAATAACACCACTCTGAAAAATATGA	953
Db	1552	CAGTCCATCAATCAACACCCCGACCGATATGA	1586
RESULT 10			
US-10-735-461-21			
; Sequence 21, Application US/10735461			
; Publication No. US20050014264A1			
; GENERAL INFORMATION:			
; APPLICANT: CZECH, Michael P.			
; APPLICANT: ZHOU, Qionghin			
; APPLICANT: JIANG, Zhen			
; TITLE OF INVENTION: METHOD OF INTRODUCING sirNA INTO			
; TITLE OF INVENTION: ADIPOCYTES			
; FILE REFERENCE: UMY-055			
; CURRENT APPLICATION NUMBER: US/10/735,461			
; CURRENT FILING DATE: 2003-12-11			
; PRIOR APPLICATION NUMBER: 60/432427			
; PRIOR FILING DATE: 2002-12-11			
; NUMBER OF SEQ ID NOS: 141			
; SOFTWARE: FastSeq for Windows Version 4.0			
; SEQ ID NO 21			
; LENGTH: 1741			
; TYPE: DNA			
; ORGANISM: Mus musculus			
US-10-735-461-21			
Query Match 53.9%; Score 527; DB 8; Length 1741;			
Best Local Similarity 72.7%; Pred. No. 3.3e-131;			
Matches 680; Conservative 0; Mismatches 255; Indels 0; Gaps 0;			
Qy	19	AGAAAGACAATGAATGATTTTGACTATTTCGAACCTACTAGTAAAGGCACCTTTTGGGAAA	78
Db	652	AAAGTGACCAATGAATGACTTCGATTATCTCAACTCTCTCGCAAGGCGACCTTCGGCAAG	711
Qy	79	GTTATTTTGGTTCGAGAGAAAGCGAAGTGGAAAAATACATGATCTATGAAGATTCGAAGAAA	138
Db	712	GTCAATTCGTGTCGAGAGAAAGCCACTGGCGGCTATTATGCCATGAAGATCCTCGCGCAAG	771
Qy	139	GAAGTCATATTTCGAAAGGATGAAGTGGCACACACCTCTAATCTGAAGCAGAGATATTAAAG	198
Db	772	GAGGTCAATCATGCAAAAGGATGAAGTCGCCCACACACAGTCACAGAGAGCCGGGTTCTGCAG	831
Qy	199	AACACTAGACATCCCTTTTAAATCCTTGAATATTCCTTCCAGACAAAGACCGTTTG	258
Db	832	AATACCAAGCACCCCTTCCTTACAGCCCTCAAGTATGCCCTCCAGACCCCATGACCCGCTA	891
Qy	259	TGTTTTGTGATGGAATATGTTAATGGGGCGAGCTGTTTTTCCATTTGTTCAGAGAGCGG	318
Db	892	TGCTTTGTGATGGATATGCCAAGGGGTGAGCTGTTTTTCCACCTCTCTCGGAGCGGA	951
Qy	319	GTGTTCTCTCAGGACCGCACACCGTTTCTATGGTGCAGAAATGTTGTTCTGCTTGGACTAT	378
Db	952	GTCTTCACGAGGATCGGGCGCGCTTTATATGGAGCAGAGATTGTTGTCAGCTCTCGAGTAT	1011
Qy	379	CTACATCCCGAAAGATTGTGTACCGTGATCTCAAGTTGGAGATCTAATGCTCGACAAA	438
Db	1012	TTGCACCTCGAGAGATGTGGTGTATCCCGTGACATCAAGCTGGAACCTTATGTTTCGACAA	1071
Qy	439	GATGGCCACATAAAATTTACAGATTTTTTGGACTTTTGAAGAAGGGATCAACAGATGCGACCC	498
Db	1072	GATGGCCACATCAAGATCACTGACTTTTGGCTTTGTGCAAGAGGGCATCAGTGATGGAGCC	1131
Qy	499	ACCATGAAGACATTTCTGTGGCACTCCAGAAATATCTGGCACACAGAGGTGTTTAGAAGATAAAT	558
Db	1132	ACCATGAAACCTTCTCTGTGTACCCCGGAGTACTTGGCGCTGAGGTGCTAGAGGACAAAT	1191
Qy	559	GACTATGGCCGACAGTAGACTGGTGGGGCCTAGGGTTGTCAATGATGAATCATGTGT	618
Db	1192	GACTATGGGGGACAGTGGACATGGTGGGGGCTGGGTGTGTTGTTGTTGATGAGATATGTGT	1251

Qy 619 GGAAGTTACCTTTCTCAACACGAGCAATGAGAAAATTTTGAATTAATTAATGAA 678  
Db 1252 GCGCGCTGCCATTTCAACACGAGCACAGCGCTCTTTGAGCTCATTTTATGGAG 1311  
Qy 679 GACATTAATTTCTCGAAGCACTCTCTTCAGATGCAAAATCATTTGCTTTAGGGCTTTG 738  
Db 1312 GAGATCCGCTTCCCGCGCACACTCGGCCAGAGGCCAAGTCCCTGCTGGCTGGAAGTCTG 1371  
Qy 739 ATAAGGATCCAAATAAACGCTTTGGTGGAGGACAGATGATGACAAAGAAAATTTATGAGA 798  
Db 1372 AAGAAGACCCAAAGCAGAGCTCGCGGAGGTCCTCAGTGAATGCAAGGAGGTCATGGAG 1431  
Qy 799 CACAGTTTCTTCTCGGAGTAAACTGGCAAGATGATATATGATATAAAAGCTTTGACCTCCT 858  
Db 1432 CATAGATTTCTTCTCAGCATCAACTGGCAGGACGCTGTACAGAAAAGCTCTGCGCACCC 1491  
Qy 859 TTTAAACCTCAAGTAAACATCTGACACAGATCTAGATATTTTGTATGAAGAATTTACAGCT 918  
Db 1492 TTCAACCTCAGGTCACTTCAGAAAGTGGACACAAAGGTACTTTGATGACGAGTTTCACCGCC 1551  
Qy 919 CAGACTATTACAATAACACCACTGAAAAATATGA 953  
Db 1552 CAGTCCATCAATACACCCCGACCGATATGA 1586

RESULT 11

US-10-895-225A-57  
; Sequence 57, Application US/10895225A  
; Publication No. US20050048587A1  
; GENERAL INFORMATION:  
; APPLICANT: Rao, Patricia  
; APPLICANT: Snyder, Jessica  
; APPLICANT: Bagley, Andrea  
; TITLE OF INVENTION: METHODS FOR IDENTIFYING TOLERANCE  
; TITLE OF INVENTION: MODULATORY COMPOUNDS AND USES THEREFOR  
; FILE REFERENCE: TILN-025  
; CURRENT APPLICATION NUMBER: US/10/895,225A  
; CURRENT FILING DATE: 2004-07-19  
; PRIOR APPLICATION NUMBER: 60/488,502  
; PRIOR FILING DATE: 2003-07-17  
; NUMBER OF SEQ ID NOS: 161  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 57  
; LENGTH: 3010  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-895-225A-57

Query Match 53.9%; Score 527; DB 9; Length 3010;  
Best Local Similarity 72.7%; Pred. No. 4.4e-131;  
Matches 680; Conservative 0; Mismatches 255; Indels 0; Gaps 0;  
Qy 19 AGAAGACATGAATGATTTTGACTATTGAACTACTAGTAAAGGCACTTTGGGAAA 78  
Db 622 AAAGTGACCATGAATGATCTTCGATTATCTCAAACTCTCGGCAAGGCGCACTTCGGCAAG 681  
Qy 79 GTTATTTGGTTCGAGAGAAGGCAAGTGGAAAATACTATGCTATGAAGATTCTGAAGAAA 138  
Db 682 GTCATTCGGTTCGAGAGAAGGCACTGGCCGCTATTATGCCATGAAGATCTTCGCGCAAG 741  
Qy 139 GAAGTCATTTGCAAAAGGATGAAGTGGGCACACACTCTAACTGAAAGCAGAGTATTAAG 198  
Db 742 GAGTTCATTTGCAAAAGGATGAAGTGGCCACACAGTCACAGAGAGCCGGTTCTCGAG 801  
Qy 199 AACACTAGACATCCCTTTTAAACATCTCTGAAATATTCCTTCCAGACAAAGACCGTTG 258  
Db 802 AATACCAAGGCAACCCCTTCTTACAGCCCTCAAGTATGCTTCCAGACCCATGACCGCTA 861  
Qy 259 TGTTTTGTGATGAATATGTTAAATGGGGCGGAGCTGTTTTTCCATTTGTTCGAGAGCGG 318  
Db 862 TGCCTTGTGATGGAGTAGTGCACAGGGGGTGAGCTGTTTTTCCACCTCTCTCGGAGCGA 921  
Qy 319 GTGTTCTCTGAGGACCGCACACGTTTCTATGGTGCAGAAAATTTGCTCTGCGCTTGGACTAT 378

Db 922 GTCTTCACGAGGATCGGCGCGCTTTATGAGCAGAGATTGTCAGCTCTGGAGTAT 981  
Qy 379 CTACATTCGGAAGAGATTGTTACCGTGATCTCAAGTTTGAGATCTAATCTGGAACA 438  
Db 982 TTGACCTCGAGAGATGTTGTTATCCCGTGACATCAAGCTGGAACCTTATGTTGGAACA 1041  
Qy 439 GATGGCCACATAAAATTTACAGATTTTGGACTTTGCAAGAGGGATCAAGATGACAGCC 498  
Db 1042 GATGGCCACATCAAGATCACTGACTTTGGCTTTGCAAGAGGGCATCAGTGATGGAGCC 1101  
Qy 499 ACCATGAAGACATTTCTGTGGCACTCCAGAAATATCTGGCACAGAGGTGTTAGAAATAT 558  
Db 1102 ACCATGAAGACCTTCTGTGGTACCCCGGAGTACTTGGCGCTCAGGTGCTAGAGACAAT 1161  
Qy 559 GACTATGGCCGACAGTACAGTGGTGGGCTTAGGGTTGTCATGTATGAATGATCTGT 618  
Db 1162 GACTATGGCGGACAGTGGACTGGTGGGCTGGGTGTCATGTATGAGATGATGTGT 1221  
Qy 619 GGGAGGTTTACCTTTCTACAAACAGGACCATGAGAAAATTTTGAATTAATTAATGAA 678  
Db 1222 GCGCGCTGCCATTTCTACAAACAGGACCAAGCGCTCTTTGAGCTCATTTATGGAG 1281  
Qy 679 GACATTAATTTCTCGAAGCACTCTCTTCAGATGCAAAATCATTTGCTTTAGGGCTTTG 738  
Db 1282 GAGATCCGCTTCCCGCGCACACTCGGCGCCAGAGGCCAAAGTCCCTGCTGGCTGGAAGTCTG 1341  
Qy 739 ATAAAGGATCCAAATAAAACGCTTTGGTGGAGGACAGATGATGACAAAGAAAATTTATGAGA 798  
Db 1342 AAGAAGACCCAAAGCAGAGGCTCGCGGAGGTCCTCAGTATGCGAAGGAGGTCATGGAG 1401  
Qy 799 CACAGTTTCTTCTCGAGTAAACTGGCAAGATGATATGATATAAAAGCTTTGACCTCCT 858  
Db 1402 CATAGATTTCTTCTCAGCATCAACTGGCAGGACGTGCTACAGAAAAGCTCTGCGCACCC 1461  
Qy 859 TTTAAACCTCAAGTAAACATCTGAGACAGATCTAGATATTTTGTATGAAGAATTTACAGCT 918  
Db 1462 TTCAAACTCAGGTCACTTCAGAAAGTGGACACAAAGGTACTTTGATGACGAGTTTCACCGCC 1521  
Qy 919 CAGACTATTACAATAACACCCCTGAAAATATGA 953  
Db 1522 CAGTCCATCAATCAACCCCGACCGGATATGA 1556

RESULT 12

US-10-324-985A-5  
; Sequence 5, Application US/10324985A  
; Publication No. US20030144204A1  
; GENERAL INFORMATION:  
; APPLICANT: Spencer, David  
; TITLE OF INVENTION: Akt-based Inducible Survival Switch for Gene Therapy  
; FILE REFERENCE: P02248US1/10106761  
; CURRENT APPLICATION NUMBER: US/10/324,985A  
; CURRENT FILING DATE: 2002-12-19  
; PRIOR APPLICATION NUMBER: US 60/342,155  
; PRIOR FILING DATE: 2001-12-19  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 5  
; LENGTH: 1140  
; TYPE: DNA  
; ORGANISM: mouse  
US-10-324-985A-5

Query Match 53.7%; Score 525; DB 6; Length 1140;  
Best Local Similarity 73.4%; Pred. No. 9.1e-131;  
Matches 685; Conservative 0; Mismatches 245; Indels 3; Gaps 1;  
Qy 24 GACAATGAATGATTTTGAATTTGACTATTGAACTACTAGGTAAAGGCACTTTTGGGAAAGTTAT 83  
Db 135 GACCATGAACGAGTTTGAGTACCTGAACTACTGGGCAAGGCGCACCTTTTGGGAAAGTAT 194  
Qy 84 TTTGGTTCGAGAGAGGCAAGTGGAAAATACTATGCTATGAAGATTTCTGAAGAAAGAAGT 143

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Db 195 TCTGTGAAAGAGAGGCCACAGGCGCTACTATGCGCATGAAGATCCTCAAGAGAGGT 254
Qy 144 CATTATGCAAGAGATGAAGTGGCCACACACTCTAACTGAAGACAGAGTATTAAAGAACAC 203
Db 255 CATCGTCGCCAAGGATGAGTTGCCACACGCTTACTGAGAACCGGTGCTCGCAAGACTC 314
Qy 204 TAGACATCCCTTTTAAACATCTTGAATATTCCTTCCAGACAAAAGACCGTTGTGTT 263
Db 315 TAGGCATCCCTTCTTACGCGCCTCAAGTACTCAATCCAGACCCACGCGCTCTGCT 374
Qy 264 TGTGATGAATATGTTAAATGCGGGCGAGCTGTTTTCATTTGTCGAGAGACGGGTGT 323
Db 375 TGTATGAGTATGCCAAGCGGGCGAGCTCTTCTCCACCTGTCTGAGAGCGGTGT 434
Qy 324 CTCTGAGGACCCGACACAGTTTCTATGTTGCAAGAAATGTTCTGCTTGGACTATCTACA 383
Db 435 CTCCGAGGACCGGGCCCGCTTCTATGTTGCGGAGATTTGTCTGCGCTGGACTACTTGA 494
Qy 384 TTCGGAAGA---TTGTGTACCGTGAATCTCAAGTTGGAGATCTAATGCTGGACAAAGA 440
Db 495 CTCCGAGAGAACGTTGTTACCGGACCTGAAGCTGGAGAACCTCATGCTGGACAAAGA 554
Qy 441 TGGCCACATAAAATTTACAGATTTTGGACTTTGCAAGAGAGGATCACAGATGCGAGCCAC 500
Db 555 CGGGCACATCAAGATAACGACTTGGGCTGTGCAAGAGGGGATCAAGGATGGTGCCAC 614
Qy 501 CATGAAGACATTTCTGTGGCCTCCAGAAATATCTGGCACGAGAGTGTAGAGATAATGA 560
Db 615 TATGAAGACATTTCTGCGGAACCGGAGTACCTGCGCCCTGAGGTGCTGGAGGACACGA 674
Qy 561 CTATGCGGAGCAGTAGACTGTGTGGGCTTAGGGTGTGTCATGTATGAATGATGTGG 620
Db 675 CTACGCGCGTGCAGTGGACTGTGTGGGGGCTGGGCGTGTGATGATGATGATGTGTGG 734
Qy 621 GAGGTTACTCTTCTACACAGGACCATGAGAACTTTTGAATTAATTAATGGAAGA 680
Db 735 CGGCTGCGCTTCTACACAGGACCATGAGAACTGTTCGAGCTGATCCTCATGGAGGA 794
Qy 681 CATTAAATTTCTCGAAACACTCTCTTTCAGATGCAAAATCATTTGCTTTGAGGCTCTTGAT 740
Db 795 GATCGCTTCCGCGCACACTCGGCCCTGAGGCCAAGTCCCTGCTCTCGGGCTGCTCA 854
Qy 741 AAAGATCCAAATAAACGCTTGTGTGGAGGACAGATGATGCAAGAAATTAATGAGACA 800
Db 855 GAAAGACCTTACACAGAGGCTCGTGTGGGGCTCTGAGGATGCAAGAGGATCATGCAGCA 914
Qy 801 CAGTTTCTCTCTGGAGTAAATGCGCAAGATGTATATGAATAAAGCTGTACCTCCTTT 860
Db 915 CCGGTTCTTTTGCACATCGTGTGGCAGGATGTATGAGAAAGAGCTGAGGCCACCTTT 974
Qy 861 TAAACCTCAAGTAAACATCTGAGACAGATACTAGATATTTTGTATGAAGAAATTTACAGCTCA 920
Db 975 CAAAGCCCAAGTCACTCTGAGACTGACACACAGGTATTTTCGATGAGGAGTTTCACAGCTCA 1034
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RESULT 13

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US-11-166-990-66
; Sequence 66, Application US/11166990
; Publication No. US20050239125A1
; GENERAL INFORMATION:
; APPLICANT: Hodge, Timothy A.
; TITLE OF INVENTION: METHODS FOR GENOTYPE SCREENING
; FILE REFERENCE: 023131.41500
; CURRENT APPLICATION NUMBER: US-11/166,990
; PRIOR FILING DATE: 2005-06-24
; PRIOR APPLICATION NUMBER: 60/230,371
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 09/945,952
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; PRIOR FILING DATE: 2001-09-04
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 66
; LENGTH: 1443
; TYPE: DNA
; ORGANISM: Mus sp.
US-11-166-990-66

Query Match      53.7%; Score 525; DB 10; Length 1443;
Best Local Similarity 73.4%; Pred. No. 1e-130;
Matches 685; Conservative 0; Mismatches 245; Indels 3; Gaps 1;

Qy 24 GACATGAAATGATTTTGAATTTGAAACTACTAGTAAAGGCACCTTTTGGAAAGTTAT 83
Db 435 GACCATGAACGAGTTTGAATGACTGAAACTACTGGGCAAGGCGACCTTTTGGAAAGTTAT 494
Qy 84 TTTGTTTCGAGAGAGGCAAGTGGAAATACTATGCTATGAAGATTTCTGAAGAAAGAGT 143
Db 495 TCTGTGAAAGAGAGGCGCCACAGCGCGTACTATGCCATGAAGATCCTCAAGAGAGAGT 554
Qy 144 CATTATTGCAAGGATGAAGTGGCACACACTTAACCTGAAAGCAGAGTATTAAAGAACAC 203
Db 555 CATCGTCGCCAAGGATGAGTTGCCACACACGCTTACTGAGAACCGTGTCTGCAGAACTC 614
Qy 204 TAGACATCCCTTTTAAACATCCCTTGAATATATCTTCCAGACAAAGACCGTTTGTGTT 263
Db 615 TAGGCATCCCTTCTTACGCGCCTCAAGTACTCAATTCAGACCCACGACCGCTCTGCTT 674
Qy 264 TGTGATGGAATATGTTAATGCGGCGAGCTGTTTTCATTTGTCGAGAGCGGGTGT 323
Db 675 TGTATGAGTATGCTCAACGCGGGCGAGCTCTTCTTCACCTGTCTCGAGAGCGGTGT 734
Qy 324 CTCTGAGAGACGCGCACACGTTTCTATGTTGCGAGAAATCTCTGCTTGGACTATCTACA 383
Db 735 CTCGAGAGACCGGGCCCGCTTCTATGTTGCGGAGATTTGTCTGCGCTTGGACTTGA 794
Qy 384 TTCGGAAGA---TTGTGTACCGTGAATCTCAAGTTGAGAAATCTAATGCTGGACAAAGA 440
Db 795 CTCCGAGAGAACGTTGTTACCGGACCTCAAGCTGGAGAACCTCATGCTGGACAAAGA 854
Qy 441 TGGCCACATAAAATTAACAGATTTTGGACTTTGCAAGAGAGGATCACAGATGCGAGCCAC 500
Db 855 CGGGCACATCAAGATAACGAGACTTGGGCTGTGCAAGAGGGGGATCAAGGATGGTGCCAC 914
Qy 501 CATGAAGACATTTCTGTGGCACTCCAGAAATATCTGGCACACAGAGTGTTAGAAGATAATGA 560
Db 915 TATGAAGACATTTCTGCGGAAACGCGGAGTACTTGGCCCTGAGGTGCTGGAGGACACGA 974
Qy 561 CTATGGCCGAGCAGTGAAGTGGTGGGCTTAGGGGTTGTCATGTATGAATGATGTGG 620
Db 975 CTACGCGCGTGCAGTGGACTGTTGGGGCTGGGCGTGTGTCATGTATGAGATGATGTGG 1034
Qy 621 GAGGTTACTTTCTACACAGGACCATGAGAACTTTTGAATTAATTAATGGAAGA 680
Db 1035 CCGCTGCGCTTCTACAAACAGGACCCAGAGAGCTGTTTCGAGCTGATCCTCATGGAGGA 1094
Qy 681 CATTAAATTTCTCGAACACACTCTCTTTCAGATGCAAAATCATTTGCTTTTCAGGGCTCTTGAT 740
Db 1095 GATCGCTTCCGCGCACACTCGGCCCTGAGGCCAAGTCCCTGCTCTCGGGCTGCTCA 1154
Qy 741 AAAGATCCAAATAAACCGCTTGTGGAGGACAGATGATGCAAGAAATTTATGAGACA 800
Db 1155 GAAAGACCTTACACAGAGGCTCGGTGGGGCTCTGAGGATGCAAGGAGATCATGCAGCA 1214
Qy 801 CAGTTTCTTCTCTGGAGTAAACTGGCAAGATGTATATGATAAAGCTTGTACCTCTTT 860
Db 1215 CCGGTTCTTTTCCCAACATCGTGTGGCAGGATGTGTATGAGAAAGAGCTGAGGCCACCTTT 1274
Qy 861 TAAACCTCAAGTAAACATCTGAGACAGATACTAGATATTTTGTATGAAGAAATTTACAGCTCA 920
Db 1275 CAAAGCCCAAGTCACTCTGAGACTGACACCCAGGTATTTTCGATGAGGAGTTTCACAGCTCA 1334
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Qy 921 GACTATTACATTAACACACACCTGAAATAATGA 953
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Db 1335 GATGATCACCATCATCGCGCTGATCAAGATGA 1367

RESULT 14
US-10-324-985A-1
; Sequence 1, Application US/10324985A
; Publication No. US20030144204A1
; GENERAL INFORMATION:
; APPLICANT: Spencer, David
; TITLE OF INVENTION: Akt-Based Inducible Survival Switch for Gene Therapy
; FILE REFERENCE: P02248US1/10106761
; CURRENT APPLICATION NUMBER: US/10/324,985A
; CURRENT FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: US 60/342,155
; PRIOR FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 2626
; TYPE: DNA
; ORGANISM: mouse
US-10-324-985A-1

Query Match 53.7%; Score 525; DB 6; Length 2626;
Best Local Similarity 73.4%; Pred. No. 1.4e-130;
Matches 685; Conservative 0; Mismatches 245; Indels 3; Gaps 1;

Qy 24 GACAATGAATGATTTGACTATTTGAACTACTAGTAAAGGCACTTTTGGGAAAGTTAT 83
|||
Db 718 GACCATGAACGAGTTTGAGTACCTGAACTACTGGCAAGGGCACCTTTGGGAAAGTGAT 777

Qy 84 TTTGGTTTCGAGAGAGCGCAAGTGAATACTATGCTATGAGATTCTGAAGAAAGT 143
|||
Db 778 TCTGGTGAAGAGAGAGCGCACAGCCGCTACTATGCCATGAAGATCCTCAAGAGAGGAT 837

Qy 144 CATTATTGCAAGAGATGAAGTGGCACACACTCTAACTGAAAGCAGAGATTAAAGAACAC 203
|||
Db 838 CATCGTCGCCAAGATGAGGTTGCCACACGCTTACTGAGAACCGTCTCTGCAAGACTC 897

Qy 204 TAGACATCCCTTTTAAATATCTTGAATAATCTTCCAGACAAAGACCGTTTGTGTTT 263
|||
Db 958 TGTATGGAATATGCGCAACCGGGCGAGCTCTTCCACCTGCTCGAGAGCGCGTGT 1017

Qy 324 CTCTGAGAGCCGACACGCTTCTATGGTCAGAAATGTCTCTGCCCTTGACATCTACAC 383
|||
Db 1018 CTCCGAGGACCGGGCCGCTTCTATGGTCGAGATTGTCTGCTGCCCTGACTACTTGA 1077

Qy 384 TTCCGGAAGA ---TTGTTGTTACCTGATCTCAAGTTGGAGAACTTAATGTTGGAAGA 440
|||
Db 1078 CTCCGAGAAAGACGTTGTTGTTACCGGACCTGAAGCTGGAGAACCTCATGCTGGACAAG 1137

Qy 441 TGGCCACATATAAATTTACAGATTTTGACATTTGCAATTTGCAAGAGAGGATCACAGTCAGCCAC 500
|||
Db 1138 CGGCAATCAAGATAACGGAATTTGCGGCTGTGCAAGGAGGGGATCAAGGATGTTGTCAC 1197

Qy 501 CATGAAGACATTTCTGTGCACTCCAGAAATATCTGGCACAGAGGTGTTAGAAAGATAATGA 560
|||
Db 1198 TATGAAGACATTTCTGGGAACCGCGAGTACTTGGCCCTGAGGTGCTGGAGGACACGA 1257

Qy 561 CTATGGCCGAGCAGTATGCTGGGCGCTTATGGGTTGTCTATGATGATAATGATGTTGTTG 620
|||
Db 1258 CTACGGCGGTGCACTGGAGCTGGTGGGCGTGGCGTGTGATGATGATGATGATGTTGTTG 1317

Qy 621 GAGTTTACCTTTCTACACACGAGGACCATGAGAACTTTTGAATTAATATTAATGGAAGA 680
|||
Db 1318 CCGCTGCGCTTCTACACACGAGGACCATGAGAACTGTTGAGCTGATCTCTCATGGAGGA 1377
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Qy 681 CATTAAATTTCTTCGAACACTCTCTTCAGATGCAAAATCATTTCTTCAGGGCTCTTGTAT 740
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Db 1378 GATCCGCTTCCCGGCACACTCGGCCCTGAGGCCAAGTCCCTCTCTCCGGGCTGCTCAA 1437

Qy 741 AAAGGATCCAAATAAAGCCTTGGTGAGAGCACAGATGATGCAAAAGAAATATGAGACA 800
|||
Db 1438 GAAGGACCCCTACACAGAGGCTCGGTGGGGCTCTGAGGATGCCAAGGAGATCATGACAGA 1497

Qy 801 CAGTTTCTTCTCTGGAGTAACTGGCAAGATGATATGATAAAAGCTTGTACCTCCTTT 860
|||
Db 1498 CCGTTCTTTGCCAACATCTGTGGCAGGATGATGAGAAGAGCTGAGCCACCTTT 1557

Qy 861 TAAACCTCAAGTAACTCTGAGACAGATAGATATTTTGTGAAGAAATTTACAGCTCA 920
|||
Db 1558 CAAGCCCGAGTCACTCTGAGACTGACACGAGTATTTTCATGAGGAGTTACAGCTCA 1617

Qy 921 GACTATTACATAACACACCTCTGAAATAATGA 953
|||
Db 1618 GATGATCACCATCATCGCGCTGATCAAGATGA 1650

RESULT 15
US-10-713-678-5
; Sequence 5, Application US/10713678
; Publication No. US20040122077A1
; GENERAL INFORMATION:
; APPLICANT: Kenneth Walsh
; APPLICANT: St. Elizabeth's Medical Center
; TITLE OF INVENTION: HMG CoA Reductase Inhibitors for
; FILE REFERENCE: 49,784 (1417)
; CURRENT APPLICATION NUMBER: US/10/713,678
; CURRENT FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: US/09/590,740
; PRIOR FILING DATE: 2000-06-08
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 2626
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-713-678-5

Query Match 53.7%; Score 525; DB 7; Length 2626;
Best Local Similarity 73.4%; Pred. No. 1.4e-130;
Matches 685; Conservative 0; Mismatches 245; Indels 3; Gaps 1;

Qy 24 GACAATGAATGATTTGACTATTTGAACTACTAGTAAAGGCACTTTTGGGAAAGTTAT 83
|||
Db 718 GACCATGAACGAGTTTGAGTACCTGAACTACTGGCAAGGGCACCTTTGGGAAAGTGAT 777

Qy 84 TTTGGTTTCGAGAGAGCGCAAGTGAATACTATGCTATGAAGATTTCTGAAGAAAGT 143
|||
Db 778 TCTGGTGAAGAGAGAGCGCACAGCCGCTACTATGCCATGAAGATCCTCAAGAGAGGAT 837

Qy 144 CATTATTGCAAGAGATGAAGTGGCACACACTCTAACTGAAAGCAGAGATTAAAGAACAC 203
|||
Db 838 CATCGTCGCCAAGATGAGGTTGCCACACGCTTACTGAGAACCGTCTCTGCAAGACTC 897

Qy 204 TAGACATCCCTTTTAAATATCTTGAATAATCTTCCAGACAAAGACCGTTTGTGTTT 263
|||
Db 898 TAGGCATCCCTTCTTACGGCCCTCAAGTACTCATTCAGACCCACACCGCTCTGCTT 957

Qy 264 TGTGATGGAATATGTTAATGGGGCGAGCTGTTTTCATTGTCGAGAGAGCGGGTGT 323
|||
Db 958 TGTGATGGAATATGCGCAACCGGGCGAGCTCTTCCACCTGCTCGAGAGCGCGTGT 1017

Qy 324 CTCTGAGAGCCGACACGCTTCTATGGTCAGAAATGTCTCTGCCCTTGACATCTACAC 383
|||
Db 1018 CTCCGAGGACCGGGCCGCTTCTATGGTCGAGATTGTGCTGCCCTGACTACTTGA 1077

Qy 384 TTCCGGAAGA ---TTGTTGTTACCTGATCTCAAGTTGGAGAACTTAATGTTGGAAGA 440
|||
Db 1078 CTCCGAGAAAGACGTTGTTGTTACCGGACCTGAAGCTGGAGAACCTCATGCTGGACAAG 1137

Qy 441 TGGCCACATATAAATTTACAGATTTTGACATTTGCAATTTGCAAGAGAGGATCACAGTCAGCCAC 500
|||
Db 1138 CGGCAATCAAGATAACGGAATTTGCGGCTGTGCAAGGAGGGGATCAAGGATGTTGTCAC 1197

Qy 501 CATGAAGACATTTCTGTGCACTCCAGAAATATCTGGCACAGAGGTGTTAGAAAGATAATGA 560
|||
Db 1198 TATGAAGACATTTCTGGGAACCGCGAGTACTTGGCCCTGAGGTGCTGGAGGACACGA 1257

Qy 561 CTATGGCCGAGCAGTATGCTGGGCGCTTATGGGTTGTCTATGATGATAATGATGTTGTTG 620
|||
Db 1258 CTACGGCGGTGCACTGGAGCTGGTGGGCGTGGCGTGTGATGATGATGATGATGTTGTTG 1317

Qy 621 GAGTTTACCTTTCTACACACGAGGACCATGAGAACTTTTGAATTAATATTAATGGAAGA 680
|||
Db 1318 CCGCTGCGCTTCTACACACGAGGACCATGAGAACTGTTGAGCTGATCTCTCATGGAGGA 1377
```

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Db 1078 CTCGAGAGACGTGGTGTTACCGGGACCTGAAGCTGGAGAACCTCATGCTGGACAAGGA 1137
QY 441 TGGCCACATPAAAAATTACAGATTTTGGACTTTGCAAGAAAGGATCACAGATGCAGCCAC 500
Db 1138 CGGGCACATCAAGATAACCGACTTCGGGCTGTGCAAGGAGGGGATCAAGGATGTGTCAC 1197
QY 501 CATGAGACATTTCTGGGACCTCCAGATATCTGGCACCCAGAGGTGTTAGAGATAATGA 560
Db 1198 TATGAAGACATTTCTGCGGAACCCCGAGTACCTGGCCCCGTGAGGTGCTGGAGGACAAGGA 1257
QY 561 CTATGGCCGAGCAGTAGACTGTGTGGGGCTTAGGGGTTGTGATGATGAAATGATGTGTGG 620
Db 1258 CTACGGCCGTGAGTGTGCTGTGGGGCTGTGGCGTGTGTCATGATGAGATGATGTGTGG 1317
QY 621 GAGGTACCTTTCTACAAACAGGACCATGAGAAACTTTTGTGAATTAATTAATGGAAGA 680
Db 1318 CGGCTGTGCTTCTACAAACAGGACCATGAGAAAGCTGTCGAGCTGATCCTCATGGAGGA 1377
QY 681 CATTAAATTTCTCGAAGACTCTCTTCAGATGCAAAATCATTTGCTTTCAGGGCTCTTGAT 740
Db 1378 GATCGGCTTCCCGCGACACTCGGGCCCTGAGGCCAAGTCCCTGCTCTCGGGCTGCTCAA 1437
QY 741 AAAGGATCCAAATAAAGCGCTTTGGTGGAGGACACAGATGATGCAAAAGAAATTAAGAGCA 800
Db 1438 GAAGGACCTTACAGAGGCTCGTGGGGGCTCTGAGGATGCCAAGGAGATCATGCAGCA 1497
QY 801 CAGTTTCTTTCTGGAGTAACTGGCAAGATGATATATGATAAAAGCTTTGTACCTCCTTT 860
Db 1498 CCGGTTCTTTGCCAACATCGTGTGGCAGGATGTGTATGAGAAGAAGCTGAGGCCACCTTT 1557
QY 861 TAAACCTCAAGTAACATCTGAGACAGATCTAGATATTTTGTATGAAGAATTTACAGCTCA 920
Db 1558 CAAGCCCCAGGTCACTCTGAGACTGACACCAAGGTATTTTCGATGAGGAGTTCCACAGCTCA 1617
QY 921 GACTATTACAATAACACCACTGAAATAATGA 953
Db 1618 GATGATCACCATCACGCCGCTGATCAAGATGA 1650
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Search completed: February 15, 2006, 09:30:20  
Job time : 860 secs

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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 15, 2006, 04:46:41 ; Search time 633 Seconds  
(without alignments)  
10297.108 Million cell updates/sec

Title: US-10-601-311-2

Perfect score: 978  
Sequence: 1 tctcaaccatcataaaag.....atggtatggactgcatggac 978

Scoring table: IDENTITY\_NUC

Gapop 10\_0 , Gapext 1.0

Searched: 4996997 seqs, 332346308 residues

Total number of hits satisfying chosen parameters: 993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- N\_Geneseq\_21:\*
- 1: Geneseqn1980s:\*
  - 2: Geneseqn1990s:\*
  - 3: Geneseqn2000s:\*
  - 4: Geneseqn2001as:\*
  - 5: Geneseqn2001bs:\*
  - 6: Geneseqn2002as:\*
  - 7: Geneseqn2002bs:\*
  - 8: Geneseqn2003as:\*
  - 9: Geneseqn2003bs:\*
  - 10: Geneseqn2003cs:\*
  - 11: Geneseqn2003ds:\*
  - 12: Geneseqn2004as:\*
  - 13: Geneseqn2004bs:\*
  - 14: Geneseqn2005s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	978	100.0	1440	3	AAAG2451	AAAG2451 Human Akt
2	978	100.0	1440	3	ABL50839	ABL50839 Human Akt
3	978	100.0	1547	3	AAAG2450	AAAG2450 Human Akt
4	978	100.0	1547	12	ADN71939	ADN71939 Human ser
5	978	100.0	1547	13	ADT99288	ADT99288 Human Akt
6	978	100.0	2367	3	AAC61592	AAC61592 DNA encod
7	978	100.0	2811	10	ADC26888	ADC26888 DNA encod
8	978	100.0	2811	13	ADQ88265	ADQ88265 Human 141
9	976.4	99.8	3285	3	AAC77341	AAC77341 Human ORF
10	949.8	97.1	1570	3	AAH96637	AAH96637 DNA encod
11	949.8	97.1	1570	4	AAD79025	AAD79025 Human Akt
12	949.8	97.1	1570	4	AAH89264	AAH89264 Human ser
13	949.8	97.1	1570	12	ADG85244	ADG85244 Human Chr
14	949.8	97.1	1703	14	ADZ49363	ADZ49363 Insulin s
15	604.2	61.8	2277	13	ADN71941	ADN71941 Chicken s
16	527	53.9	1722	13	ABD33334	ABD33334 Murine ca
17	527	53.9	1741	10	ADC26886	ADC26886 DNA encod
18	527	53.9	1741	12	ADP48781	ADP48781 Mouse Akt
19	527	53.9	3010	14	ADX01484	ADX01484 Human tol

20	525	53.7	1140	10	ADC26889	ADC26889 DNA encod
21	525	53.7	2626	3	AAA09078	AAA09078 Wild type
22	525	53.7	2626	6	AAD28550	AAD28550 Mouse Akt
23	525	53.7	2626	10	ADC26885	ADC26885 DNA encod
24	525	53.7	2626	12	ADP48780	ADP48780 Mouse Akt
25	525	53.7	2626	14	ADX01483	ADX01483 Human tol
26	525	53.7	6891	12	ADL25356	ADL25356 ARK5 rela
27	517.4	52.9	1593	12	ADQ84311	ADQ84311 Human tum
28	517.4	52.9	1593	13	ADQ86862	ADQ86862 Human tum
29	517.4	52.9	1593	13	ADQ83643	ADQ83643 Human tum
30	517.4	52.9	1593	13	ADQ85783	ADQ85783 Human tum
31	517.4	52.9	1593	13	ACN40577	ACN40577 Tumour-as
32	517.4	52.9	2562	13	ABD33336	ABD33336 Human can
33	515.8	52.7	1446	6	ABL50838	ABL50838 Human Akt
34	515.8	52.7	1599	2	AAT71252	AAT71252 Mouse Akt
35	515.8	52.7	1599	3	AAA08448	AAA08448 Nucleotid
36	515.8	52.7	1599	3	AAG60814	AAG60814 Nucleotid
37	515.8	52.7	1599	10	ADC26887	ADC26887 DNA encod
38	515.8	52.7	1599	11	ADI31678	ADI31678 Human CDN
39	515.8	52.7	1599	12	ADN71937	ADN71937 Human pro
40	515.8	52.7	1599	13	ADS83745	ADS83745 Human lym
41	515.8	52.7	1715	6	ABV94263	ABV94263 Breast ca
42	515.8	52.7	1715	12	ADP48783	ADP48783 Human Akt
43	515.8	52.7	1715	14	ADZ26090	ADZ26090 Human gen
44	515.8	52.7	3897	13	ACN43263	ACN43263 Human dia
45	512.2	52.4	2729	14	ADX01463	ADX01463 Human tol

ALIGNMENTS

RESULT 1

AAAG2451  
ID AAAG2451 standard; cDNA; 1440 BP.

XX

AC AAAG2451;

XX

DT 13-NOV-2000 (first entry)

XX Human Akt-3 coding sequence.

DE

XX Human; Akt-3; protein kinase B; PKB; serine/threonine kinase; cytosolic;  
KW apoptosis stimulator; cancer; rapid amplification of cDNA ends; RACE;  
KW chromosome 1q43-44; ss.

XX Homo sapiens.

OS

XX Key Location/Qualifiers

FT CDS 1..1440

FT /\*tag= a

FT /product= "Akt-3"

XX

XX WO200037613-A2.

XX

PD 29-JUN-2000.

XX

PF 17-DEC-1999; 99WO-GB004311.

XX

PR 22-DEC-1998; 98GB-00028375.

XX

PA (JANC ) JANSEN PHARM NV.

XX

PI Masure SLJ, Richardson A;

XX

DR WPI; 2000-498840/44.

DR P-PSDB; AAB13393.

XX

PT New human serine/threonine kinase protein and the polynucleotide encoding  
the protein, useful for preparing a medicament for treating disorders  
associated with human serine/threonine kinase protein activity,  
especially cancer.

PS Claim 4; Fig 1; 61pp; English.

XX The present sequence is the coding region of the nucleotide sequence that  
 CC encodes human Akt-3. Akt-3 is a third human isoform of Akt, which is also  
 CC known as protein kinase B (PKB) or "related to A and C protein kinase"  
 CC (RAC-PK). The gene encoding Akt-3 is located on human chromosome 1,  
 CC region q43-q44. A human hippocampal EST sequence that showed high  
 CC similarity to the rat RAC-PKgamma sequence was used to design primers for  
 CC 3' rapid amplification of cDNA ends (3' RACE). The sequence obtained in  
 CC the first round of 3' RACE was used to design primers for a second round.  
 CC The complete sequence was then amplified from human hippocampal cDNA by  
 CC PCR using primers based on the product of the second round of 3' RACE.  
 CC Akt can inhibit apoptosis induced by detachment from the extracellular  
 CC matrix. The Akt-3 nucleic acid molecule and protein may be used as  
 CC medicaments for treating cancer. Agents which influence the activity of  
 CC Akt-3 protein, and so stimulate apoptosis, may also be used to treat  
 CC diseases associated with Akt-3  
 XX  
 SQ Sequence 1440 BP; 489 A; 248 C; 330 G; 373 T; 0 U; 0 Other;

Query Match 100.0%; Score 978; DB 3; Length 1440;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-257;  
 Matches 978; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCTACACCCATCATAAAGAAAGACACATGAATGATTTTGACTATTGAAACTACTAGGT 60  
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
 Qy 406 TCTACACCCATCATAAAGAAAGACACATGAATGATTTTGACTATTGAAACTACTAGGT 465  
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 61 AAAGCGACTTTTGGAAAGTTATTGTTGTCGAGAGAGGCAAGTGGAAATATCTATGCT 120  
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 466 AAAGCGACTTTTGGAAAGTTATTGTTGTCGAGAGAGGCAAGTGGAAATATCTATGCT 525  
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 121 ATGAAGATTCTGAAGAAAGAGTCAATATTGCAAGGATGAAGTGGCACACACTCTAACT 180  
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 526 ATGAAGATTCTGAAGAAAGAGTCAATATTGCAAGGATGAAGTGGCACACACTCTAACT 585  
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 181 GAAAGCAGAGTATTAAAGAACACTAGACATCCCTTTTAAACATCCTTGAATATTCCTTC 240  
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 586 GAAAGCAGAGTATTAAAGAACACTAGACATCCCTTTTAAACATCCTTGAATATTCCTTC 645  
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 241 CAGACAAAGACCGTTGTGTTTGTATGGAATATGTTAATGGGCGAGCTGTTTTC 300  
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 646 CAGACAAAGACCGTTGTGTTTGTATGGAATATGTTAATGGGCGAGCTGTTTTC 705  
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 301 CATTTGTGCGAGAGCGGGTCTCTGAGGACGCGACACCGTTTCTATGGTGCAAAAT 360  
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 706 CATTTGTGCGAGAGCGGGTCTCTGAGGACGCGACACCGTTTCTATGGTGCAAAAT 765  
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 361 GTCTCTGCGTTGGACTATCTACATTCGGAAAGATTGTGTACCGTGATCTCAAGTTGGAG 420  
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 766 GTCTCTGCGTTGGACTATCTACATTCGGAAAGATTGTGTACCGTGATCTCAAGTTGGAG 825  
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 421 AATCTAATGCTGGACAAAGATGGCCACATAAAATACAGATTTTGGACTTTGCAAAAGAA 480  
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 826 AATCTAATGCTGGACAAAGATGGCCACATAAAATACAGATTTTGGACTTTGCAAAAGAA 885  
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 481 GGGATCAGATGCGAGCCACCACCAAGACATTTCTGTGCACTCCAGCAATATCTGCGACCA 540  
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 886 GGGATCAGATGCGAGCCACCACCAAGACATTTCTGTGCACTCCAGCAATATCTGCGACCA 945  
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 541 GAGGTGTTAGAAGATATGACTATGGCGGACGATAGACTGGTGGGCGCTAGGGGTTGTC 600  
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 946 GAGGTGTTAGAAGATATGACTATGGCGGACGATAGACTGGTGGGCGCTAGGGGTTGTC 1005  
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 601 ATGTATGAATGATGCTGGGAGGTACCTTTCTACACACGAGGACCATGAGAACTTTT 660  
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 1006 ATGTATGAATGATGCTGGGAGGTACCTTTCTACACACGAGGACCATGAGAACTTTT 1065  
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 661 GAATTAATATTAATGAAGACATTAATTTCTCGAACACTCTCTTCAGATGCAAAATCA 720  
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 1066 GAATTAATATTAATGAAGACATTAATTTCTCGAACACTCTCTTCAGATGCAAAATCA 1125  
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 721 TTGCTTTTCAGGGCTCTTGATTAAGATTCCTAAATAAACCGCTTGTGTGAGGACCAAGATGAT 780  
 Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Db 1126 TTGCTTTTCAGGGCTCTTGATAAAGGATCCAAATAAACGCCCTTGCTGGAGGACCAGATGAT 1185  
 Qy 781 GCAAAAGAAATTTAGACACACAGTTTCTCTCTGAGTAAACTGCGAAGATGTATATGAT 840  
 Db 1186 GCAAAAGAAATTTAGACACACAGTTTCTCTCTGAGTAAACTGCGAAGATGTATATGAT 1245  
 Qy 841 AAAAAGCTTTGATCCCTCTTTTAAACCTCAAGTAAACATCTGAGACAGATATCTAGATATTTT 900  
 Db 1246 AAAAAGCTTTGATCCCTCTTTTAAACCTCAAGTAAACATCTGAGACAGATATCTAGATATTTT 1305  
 Qy 901 GATGAAGATTTACAGCTCAGACTTATTAACATTAACACACCTGAAATAATATGATGAGAT 960  
 Db 1306 GATGAAGATTTACAGCTCAGACTTATTAACATTAACACACCTGAAATAATATGATGAGAT 1365  
 Qy 961 GGTATGACATGCGATGGAC 978  
 Db 1366 GGTATGACATGCGATGGAC 1383

RESULT 2  
 ABL50839  
 ID ABL50839 standard; cDNA; 1440 BP.  
 XX  
 AC ABL50839;  
 XX  
 DT 20-JUN-2002 (first entry)  
 XX  
 DE Human Akt3 encoding cDNA SEQ ID NO:10.  
 XX  
 KW Human; Hsp90 beta; Hsp90 alpha; Akt1; Akt2; Akt3; apoptosis regulation;  
 KW apoptotic; serine/threonine kinase; heat shock protein; anticancer;  
 KW cytosolic; cardiant; vasotropic; hepatotropic; neuroprotective;  
 KW antidiabetic; nootropic; cancer; diabetes; Alzheimer's disease;  
 KW cell death; radiation; brain ischaemia; cardiac ischaemia; gene; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 CDS 1..1440  
 FT /\*tag= a  
 FT /product= "Akt3"  
 XX  
 FN WO200215925-A1.  
 XX  
 PD 28-FEB-2002.  
 XX  
 PF 22-AUG-2001; 2001WO-JP007179.  
 XX  
 PR 22-AUG-2000; 2000JP-00251529.  
 XX  
 PA (KYOW ) KYOWA HAKKO KOGYO KK.  
 PA (TSUR/) TSURUO T.  
 XX  
 PI Teuruo T, Fujita N, Sato S;  
 XX  
 DR WPI; 2002-292035/33.  
 DR P-PSDB; ABB06998.  
 XX  
 PT Regulation of apoptosis by promoting or inhibiting the intracellular  
 PT binding of Akt with Hsp90, useful for prevention and treatment of  
 PT apoptosis-regulation associated diseases including cancer.  
 XX  
 PS Disclosure; Page 87-89; 93pp; Japanese.  
 XX  
 CC The present invention describes the regulation of apoptosis, in which the  
 CC intracellular binding of Akt (a serine/threonine kinase) with Hsp90 (a  
 CC heat-shock protein) is promoted or inhibited. The present invention also  
 CC describes: (1) isoforms of Akt and Hsp90, and their partial peptides  
 CC including the binding domain; (2) antibodies to Akt or Hsp90; (3) DNA  
 CC encoding Akt or Hsp90 or their partial peptides including the binding  
 CC domain; (4) expression vectors containing the DNA; (5) host cells  
 CC transformed by the vectors; (6) production of Akt or Hsp90 or their  
 CC partial peptides including the binding domain by culture of the

transfected cells; (7) screening compounds for their ability to modify intracellular Akt activity by contact with cells expressing Akt or Hsp90; and (8) drug compositions containing antibodies recognizing the binding domain of Akt or Hsp90 and optionally also an anticancer agent. Akt and Hsp90 have cytoskeletal, cardiant, vasotropic, hepatotropic, antidiabetic, neuroprotective and nootropic activities. Blockade of the binding of Hsp90 with Akt increases the sensitivity of cells to apoptosis induction. Akt and Hsp90 can be used in the prevention and treatment of diseases with which apoptosis regulation is associated, including cancer (such as gastric cancer, ovarian cancer, breast cancer, pancreatic cancer and prostate cancer), diabetes, Alzheimer's disease, cell death caused by radiation or anticancer agents, brain ischaemia or cardiac ischaemia. The present sequence encodes human Akt3 which is used in the exemplification of the present invention

XX Sequence 1440 BP; 489 A; 248 C; 330 G; 373 T; 0 U; 0 Other;

Query Match 100.0%; Score 978; DB 6; Length 1440;

Best Local Similarity 100.0%; Pred. No. 1.3e-257;

Matches 978; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	TCTACAAACCCATCAATAAAGAAAGACAATGAATGATTTTGAATTTGAACTACTAGGT	60
Db	406	TCTACAAACCCATCAATAAAGAAAGACAATGAATGATTTTGAATTTGAACTACTAGGT	465
QY	61	AAAGGCATTTTGGGAAAGTTATTTTGGTTTCAGAGAAGCAAGTGGAAAACTATGCT	120
Db	466	AAAGGCATTTTGGGAAAGTTATTTTGGTTTCAGAGAAGCAAGTGGAAAACTATGCT	525
QY	121	ATGAAGATTCTGAAGAAGCAAGTCATTATTGTCAAAGGATGAAGTGGCACACACTCTA	180
Db	526	ATGAAGATTCTGAAGAAGCAAGTCATTATTGTCAAAGGATGAAGTGGCACACACTCTA	585
QY	181	GAAAGCAGATATTAAAGAACACTAGACATCCCTTTTAAACATCTCTTGAATATTCCTTC	240
Db	586	GAAAGCAGATATTAAAGAACACTAGACATCCCTTTTAAACATCTCTTGAATATTCCTTC	645
QY	241	CAGACAAAAGACCGTTTGTGTTTGTGATGGAATATGTTAATGGGGGCGAGCTGTTTTC	300
Db	646	CAGACAAAAGACCGTTTGTGTTTGTGATGGAATATGTTAATGGGGGCGAGCTGTTTTC	705
QY	301	CATTTGTCCAGAGAGCGGTGTTCTCTGAGGACCGCACACGTTTCTATGGTGCAGAAAT	360
Db	706	CATTTGTCCAGAGAGCGGTGTTCTCTGAGGACCGCACACGTTTCTATGGTGCAGAAAT	765
QY	361	GTCTCTGCTTGGACTATCTACATTCGGAAGATTTGTACCGTATCTCAAGTTGGAG	420
Db	766	GTCTCTGCTTGGACTATCTACATTCGGAAGATTTGTACCGTATCTCAAGTTGGAG	825
QY	421	AATCTAATGCTGGACAAAGATGCCACATAAAATTTACAGATTTTGGACTTTGCAAGAA	480
Db	826	AATCTAATGCTGGACAAAGATGCCACATAAAATTTACAGATTTTGGACTTTGCAAGAA	885
QY	481	GGGATCAGAGATGACCCACCATGAAGACATTTCTGGGACCTCCAGATATCTGGCACA	540
Db	886	GGGATCAGAGATGACCCACCATGAAGACATTTCTGGGACCTCCAGATATCTGGCACA	945
QY	541	GAGGTGTTAGAAGATAATCACTATGCCGAGCAGTAGACTGTGGGGCCCTAGGGGTTGTC	600
Db	946	GAGGTGTTAGAAGATAATCACTATGCCGAGCAGTAGACTGTGGGGCCCTAGGGGTTGTC	1005
QY	601	ATGTATGAATGATGTGGGAGGTTAATCTTTCTACACAGGACCATGAGAAACCTTTT	660
Db	1006	ATGTATGAATGATGTGGGAGGTTAATCTTTCTACACAGGACCATGAGAAACCTTTT	1065
QY	661	GAATTAATTAATGGAAGACATTAATTTCTCGAACACTCTCTTCAGATGCAAAATCA	720
Db	1066	GAATTAATTAATGGAAGACATTAATTTCTCGAACACTCTCTTCAGATGCAAAATCA	1125
QY	721	TTGCTTTTCAGGCTCTTTGATAAAGATCCAAATAAACCGCTTTGGTGGAGGACCATGAT	780
Db	1126	TTGCTTTTCAGGCTCTTTGATAAAGATCCAAATAAACCGCTTTGGTGGAGGACCATGAT	1185

QY	781	GCAAAAGAAATTTATGAGACACAGATTTCTTCTCTGGAGTAAACTGGCAAGATGTATATGAT	840
Db	1186	GCAAAAGAAATTTATGAGACACAGATTTCTTCTCTGGAGTAAACTGGCAAGATGTATATGAT	1245
QY	841	AAAAAGCTTGTACCTCCCTTTTAAACCTCAAGTAAACATCTGAGACAGATAGATATTTT	900
Db	1246	AAAAAGCTTGTACCTCCCTTTTAAACCTCAAGTAAACATCTGAGACAGATAGATATTTT	1305
QY	901	GATGAAGAATTTACAGCTCAGACTATTACAAATTAACACCACTTGAAAAATATATGATGAGAT	960
Db	1306	GATGAAGAATTTACAGCTCAGACTATTACAAATTAACACCACTTGAAAAATATATGATGAGAT	1365
QY	961	GCTATGGACTGCATGGAC	978
Db	1366	GCTATGGACTGCATGGAC	1383

RESULT 3  
AAAG62450  
ID AAAG62450 standard; cDNA; 1547 BP.  
XX  
AC AAAG62450;  
XX  
DT 13-NOV-2000 (first entry)  
XX  
DE Human Akt-3 nucleotide sequence.  
XX  
KW Human; Akt-3; protein kinase B; PKB; serine/threonine kinase; cytosolic;  
KW apoptosis stimulator; cancer; rapid amplification of cDNA ends; RACE;  
KW chromosome 1q43-44; ss.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT 11..1450  
FT /\*tag= a  
FT /product= "Akt-3"  
FT /note= "nucleotides 11 to 1447 are given as SEQ ID NO: 2  
FT in the specification and are specifically claimed in  
FT claim 4 (see AAAG62451)"  
XX  
PN WO200037613-A2.  
XX  
PD 29-JUN-2000.  
XX  
PF 17-DEC-1999; 99WO-GB004311.  
XX  
PR 22-DEC-1998; 98GB-00028375.  
XX  
PA (JANC ) JANSSEN PHARM NV.  
XX  
PI Masure SLJ, Richardson A;  
XX  
XX WPI: 2000-498840/44.  
XX P-PSDB; AAB13393.  
XX  
PT New human serine/threonine kinase protein and the polynucleotide encoding  
PT the protein, useful for preparing a medicament for treating disorders  
PT associated with human serine/threonine kinase protein activity,  
PT especially cancer.  
XX  
PS Claim 3; Fig 1; 61pp; English.  
XX  
XX The present sequence encodes human Akt-3. Akt-3 is a third human isoform  
CC of Akt, which is also known as protein kinase B (PKB) or "related to A  
CC and C protein kinase" (RAC-PK). The gene encoding Akt-3 is located on  
CC human chromosome 1, region q43-q44. A human hippocampal EST sequence that  
CC showed high similarity to the rat RAC-PKgamma sequence was used to design  
CC primers for 3' rapid amplification of cDNA ends (3' RACE). The sequence  
CC obtained in the first round of 3' RACE was used to design primers for a  
CC second round. The complete sequence was then amplified from human  
CC hippocampal cDNA by PCR using primers based on the product of the second  
CC round of 3' RACE. Akt can inhibit apoptosis induced by detachment from

CC the extracellular matrix. The Akt-3 nucleic acid molecule and protein may  
CC be used as medicaments for treating cancer. Agents which influence the  
CC activity of Akt-3 protein, and so stimulate apoptosis, may also be used  
CC to treat diseases associated with Akt-3

XX	Sequence	1547 BP; 515 A; 276 C; 348 G; 408 T; 0 U; 0 Other;
XX	Query Match	100.0%; Score 978; DB 3; Length 1547;
XX	Best Local Similarity	100.0%; Pred. No. 1.4e-257;
XX	Matches	978; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	1	TCTACAACCCATCATAAAGAAAGACAAATGAATGATTTTGACTATTGAAACTACTAGGT 60
Db	416	TCTACAACCCATCATAAAGAAAGACAAATGAATGATTTTGACTATTGAAACTACTAGGT 475
Qy	61	AAAGGCACCTTTTGGGAAAGTTATTTTTGGTTCGAGAGAGGCAAGTGGAAATACTATGCT 120
Db	476	AAAGGCACCTTTTGGGAAAGTTATTTTTGGTTCGAGAGAGGCAAGTGGAAATACTATGCT 535
Qy	121	ATGAAGATTCTGAAGAAAGAGTCAATTATTGCAAGAGATGAAGTGGCACACACTCTAACT 180
Db	536	ATGAAGATTCTGAAGAAAGAGTCAATTATTGCAAGAGATGAAGTGGCACACACTCTAACT 595
Qy	181	GAAGAGCAGATPATTAAAGAACACTAGACATCCCTTTTAAACATCCTTTGAAATATTCCTTC 240
Db	596	GAAGAGCAGATPATTAAAGAACACTAGACATCCCTTTTAAACATCCTTTGAAATATTCCTTC 655
Qy	241	CAGACAAAGACCGTTTGTGTTTGTGATGGAATATGTTAATGGGCGGAGCTGTTTTTC 300
Db	656	CAGACAAAGACCGTTTGTGTTTGTGATGGAATATGTTAATGGGCGGAGCTGTTTTTC 715
Qy	301	CATTGTGCGAGAGCGGGTCTCTCTGAGGACCGCACACATGTTTCTATGTCGACAAAT 360
Db	716	CATTGTGCGAGAGCGGGTCTCTCTGAGGACCGCACACATGTTTCTATGTCGACAAAT 775
Qy	361	GTCTCTGCTTGGACTATCTACATTCCTGGGAAAGATTGTGACCGTATCTCAAGTTGGAG 420
Db	776	GTCTCTGCTTGGACTATCTACATTCCTGGGAAAGATTGTGACCGTATCTCAAGTTGGAG 835
Qy	421	AATCTAATGCTGGACAAAGATGGCCACATAAATAATACAGATTTTGACATTTGCAAGAA 480
Db	836	AATCTAATGCTGGACAAAGATGGCCACATAAATAATACAGATTTTGACATTTGCAAGAA 895
Qy	481	GGGATCAGATGCGAGCCACCATGAAGACATTTCTGTGGCACTCCAGAAATATCTGGCACCA 540
Db	896	GGGATCAGATGCGAGCCACCATGAAGACATTTCTGTGGCACTCCAGAAATATCTGGCACCA 955
Qy	541	GAGGTGTTGAAGATAATGACTATGGCCGAGCAGTAGACTGGTGGGCGCTAGGGGTTGTC 600
Db	956	GAGGTGTTGAAGATAATGACTATGGCCGAGCAGTAGACTGGTGGGCGCTAGGGGTTGTC 1015
Qy	601	ATGTATGAAATGATGTGGGAGGTACCTTTCTACACAGGACCATGAGAACTTTTT 660
Db	1016	ATGTATGAAATGATGTGGGAGGTACCTTTCTACACAGGACCATGAGAACTTTTT 1075
Qy	661	GAATTAATATTAATGGAAGACATTAATAATTTCTCGAACACTCTCTCAGATGCAAAATCA 720
Db	1076	GAATTAATATTAATGGAAGACATTAATAATTTCTCGAACACTCTCTCAGATGCAAAATCA 1135
Qy	721	TGCTTTTCAGGGCTCTTGATAAAGATCCAAATAAAGCCCTTGTGTGGAGCCAGATGAT 780
Db	1136	TGCTTTTCAGGGCTCTTGATAAAGATCCAAATAAAGCCCTTGTGTGGAGCCAGATGAT 1195
Qy	781	GCAAAAGAAATATGAGACACAGTTTCTCTCGAGTAACTGGCAAGATGTATGAT 840
Db	1196	GCAAAAGAAATATGAGACACAGTTTCTCTCGAGTAACTGGCAAGATGTATGAT 1255
Qy	841	AAAAAGCTTGACCTCTCTTTTAAACCTCAAGTAACATCTGAGACAGATCTAGATATTTT 900
Db	1256	AAAAAGCTTGACCTCTCTTTTAAACCTCAAGTAACATCTGAGACAGATCTAGATATTTT 1315
Qy	901	GATGAAGATTTACAGCTCAGACTATTACAAATAACACACCTGAAATAATATGATGAGAT 960

Db	1316	GATGAAGATTTACAGCTCAGACTATTACAAATACACCACTGAAAAATATGATGAGAT 1375
Qy	961	GGTATGGACTGCATGGAC 978
Db	1376	GGTATGGACTGCATGGAC 1393
RESULT 4		
ADN71939		
ID	ADN71939	standard; cDNA; 1547 BP.
XX	AC	ADN71939;
XX	DT	12-AUG-2004 (first entry)
XX	DE	Human serine/threonine kinase Akt-3 encoding cDNA SEQ ID NO:25.
XX	KW	kinase pathway inhibitor; anti-prostate cancer;
KW		mitogen-activated protein kinase pathway inhibitor;
KW		MAP kinase pathway inhibitor; prostate cancer inhibitor;
KW		phosphatidylinositol 3-kinase/Akt kinase pathway;
KW		PI3K/Akt kinase pathway; cytosolic; MAP kinase inhibitor;
KW		phosphatidylinositol 3-kinase/Akt kinase inhibitor;
KW		PI3K/Akt kinase inhibitor; androgen receptor inhibitor; prostate cancer;
KW		human; serine/threonine kinase Akt-3; chromosome 1; gene; ss.
OS		Homo sapiens.
XX	Key	Location/Qualifiers
FT	CDS	11..1450
FT		/*tag= a
FT		/product= "serine/threonine kinase Akt-3"
XX		WO2004041185-A2.
XX		21-MAY-2004.
XX		31-OCT-2003; 2003WO-US034636.
XX		31-OCT-2002; 2002US-0423340P.
XX		(UYRP ) UNIV ROCHESTER.
XX		Chang C, Lee Y, Lin W;
XX		WPI; 2004-390508/36.
DR		P-PSDB; ADN71940.
XX		Composition useful in the treatment of e.g. prostate cancer comprises a kinase pathway inhibitor and an anti-prostate cancer compound.
XX		Disclosure; SEQ ID NO 25; 118pp; English.
XX		The present invention describes a composition (C1) which comprises a kinase pathway inhibitor (a) and an anti-prostate cancer compound (b).
CC		Also described: (1) identification of a mitogen-activated protein (MAP) kinase pathway inhibitor involving incubating an antiandrogen or a library of molecules with a cell containing an activable MAP kinase pathway and selecting the molecules which inhibit the activation of the MAP kinase pathway; and (2) identification of a prostate cancer inhibitor involving incubating a cell with hydroxyflutamide and potential inhibitor, and assaying the level of activation of MAP kinase pathway or phosphatidylinositol 3-kinase (PI3K)/Akt kinase pathway. C1 has cytosolic activity, and can be used as a MAP kinase inhibitor.
CC		phosphatidylinositol 3-kinase (PI3K)/Akt kinase inhibitor, and androgen receptor (AR) inhibitor. C1 can be used in the treatment of prostate cancer; for identifying a MAP kinase pathway inhibitor; for identifying a prostate cancer inhibitor; and for reducing the number of prostate cancer cells in a sample. The composition C1 provides effective combination therapy as compared to prior therapies. The present sequence encodes human serine/threonine kinase Akt-3, which is used in the exemplification of the present invention.
XX		

SQ	Sequence 1547 BP; 515 A; 276 C; 348 G; 408 T; 0 U; 0 Other;	
Query Match	100.0%; Score 978; DB 12; Length 1547;	
Best Local Similarity	100.0%; Pred. No. 1.4e-257;	
Matches 978; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1 TCTACAACCCATCATAAAGAAAGCAATGAATGATTTTGACTATTTGAAACTACTAGGT 60	XX ADT99288 standard; cDNA; 1547 BP.
DB	416 TCTACAACCCATCATAAAGAAAGCAATGAATGATTTTGACTATTTGAAACTACTAGGT 475	XX ADT99288;
QY	61 AAAGGCACCTTTTGGGAAAGTATTTTGGTTTCGAGAGAGGCAAGTGGAAATACTATGCT 120	XX ADT99288; (first entry)
DB	476 AAAGGCACCTTTTGGGAAAGTATTTTGGTTTCGAGAGAGGCAAGTGGAAATACTATGCT 535	XX Human Akt3 cDNA.
QY	121 ATGAAGATTTCTGAAGAAAGAACTATTAATGCAAAAGGATGAAGTGGCACACACTCTAACT 180	XX Akt3; Akt3 inhibitor; tumour; cancers; atherosclerosis; psoriasis;
DB	536 ATGAAGATTTCTGAAGAAAGAACTATTAATGCAAAAGGATGAAGTGGCACACACTCTAACT 595	XX autoimmune diseases; bacterial infection; viral infection; HIV infection;
QY	181 GAAAGCAGAGTATTAAAGAAACACTAGACATCCCTTTTAAACATCTTGAATATTTCCCTTC 240	XX hepatitis; antiarteriosclerotic; antibacterial; anti-HIV;
DB	596 GAAAGCAGAGTATTAAAGAAACACTAGACATCCCTTTTAAACATCTTGAATATTTCCCTTC 655	XX antiinflammatory; antipsoriatic; cytostatic; hepatotropic;
QY	241 CAGACAAAAGACCGTTTGTGTTTGTGATGGAATATGTTAATGGGGCGAGCTGTTTTTC 300	XX immunosuppressive; virucide; human; protein kinase B; ss.
DB	656 CAGACAAAAGACCGTTTGTGTTTGTGATGGAATATGTTAATGGGGCGAGCTGTTTTTC 715	XX Homo sapiens.
QY	301 CATTTGTCGAGAGCGGGTGTCTCTGAGACCGCACACGTTTCTATGGTCGCAAAAT 360	XX OS
DB	716 CATTTGTCGAGAGCGGGTGTCTCTGAGACCGCACACGTTTCTATGGTCGCAAAAT 775	XX XX
QY	361 GTCTCTGCTTGACTATCTACATTTCCGGAAGATGTGTACCGTGATCTCAAGTTGGAG 420	XX PN US6809194-B1.
DB	776 GTCTCTGCTTGACTATCTACATTTCCGGAAGATGTGTACCGTGATCTCAAGTTGGAG 835	XX PD 26-OCT-2004.
QY	421 AATCTAATGCTGCAACAAAGATGCCACATAAAATTTACAGATTTTGGACTTTGCAAGAA 480	XX PF 08-MAY-2001; 2001US-00851670.
DB	836 AATCTAATGCTGCAACAAAGATGCCACATAAAATTTACAGATTTTGGACTTTGCAAGAA 895	XX PR 10-MAY-2000; 2000US-0203543P.
QY	481 GGGATCACAGATGCGACCCACCAATGAAGACATTTCTGTGGCACTCCAGAAATATCTGGCACCA 540	XX PA (CHIR ) CHIRON CORP.
DB	896 GGGATCACAGATGCGACCCACCAATGAAGACATTTCTGTGGCACTCCAGAAATATCTGGCACCA 955	XX PI Reinhard C, Jefferson AB;
QY	541 GAGGTGTTAGAAGATAATGACTATGCGCAGAGTAGACTGTGGGGCTTAGGGGTTGTTC 600	XX XX WPI; 2004-755774/74.
DB	956 GAGGTGTTAGAAGATAATGACTATGCGCAGAGTAGACTGTGGGGCTTAGGGGTTGTTC 1015	PT New Akt3 inhibitor, useful for treating cancer, atherosclerosis,
QY	601 ATGTATGAATCATGTGTGGGAGGTTTACCTTTCTCAACCGAGCACCATGAGAACTTTT 660	XX psoriasis, autoimmune diseases, and bacterial and viral infections.
DB	1016 ATGTATGAATCATGTGTGGGAGGTTTACCTTTCTCAACCGAGCACCATGAGAACTTTT 1075	XX Example 1; SEQ ID NO 1; 23pp; English.
QY	661 GAATTAATATTAAATGGAAGACATTAATTTCTCGAACACTCTCTTTCAGATGCAAAATCA 720	XX The present invention relates to an Akt3 inhibitor, where the inhibitor
DB	1076 GAATTAATATTAAATGGAAGACATTAATTTCTCGAACACTCTCTTTCAGATGCAAAATCA 1135	XX is an antisense molecule capable of inhibiting the expression of human
QY	721 TTGCTTTTACGGCTCTTGATAAAGNATCCAAATAAAGCGCTTGTGGAGGACCAAGATGAT 780	XX Akt3. The Akt3 inhibitor is useful for preparing a medicament for
DB	1136 TTGCTTTTACGGCTCTTGATAAAGNATCCAAATAAAGCGCTTGTGGAGGACCAAGATGAT 1195	XX modulating cell proliferation and for treating tumours, cancers,
QY	781 GCAAAAGAAATATTAGACACACAGTTTCTTCTCTGGAGTAAACTGGCAAGATGTATATGAT 840	XX atherosclerosis, psoriasis, autoimmune diseases, bacterial infections and
DB	1196 GCAAAAGAAATATTAGACACACAGTTTCTTCTCTGGAGTAAACTGGCAAGATGTATATGAT 1255	XX viral infections like human immunodeficiency virus 1 (HIV) infections or
QY	841 AAAAGCTTTGTACCTCTTTTAAACCTCAAGTAAACATCTGAGACAGATACTAGATATTTT 900	XX hepatitis. The present sequence is the human Akt3 cDNA. Akt3 is also
DB	1256 AAAAGCTTTGTACCTCTTTTAAACCTCAAGTAAACATCTGAGACAGATACTAGATATTTT 1315	XX known as protein kinase B.
QY	901 GATGAAGAAATTTACAGCTCAGACTATTAACAATAACACCTGMAAAATATGATGAGGAT 960	SQ Sequence 1547 BP; 515 A; 276 C; 348 G; 408 T; 0 U; 0 Other;
DB	1316 GATGAAGAAATTTACAGCTCAGACTATTAACAATAACACCTGMAAAATATGATGAGGAT 1375	Query Match 100.0%; Score 978; DB 13; Length 1547;
QY	961 GGTATGGACTGCATGGAC 978	Best Local Similarity 100.0%; Pred. No. 1.4e-257;
DB	1376 GGTATGGACTGCATGGAC 1393	Matches 978; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 301 CATTGTGCGAGAGCGGGTGTCTCTGAGGACCGCACACGTTTCTATGTCGAGAAATT 360  
Db |||||  
Qy 716 CATTGTGCGAGAGCGGGTGTCTCTGAGGACCGCACACGTTTCTATGTCGAGAAATT 775  
Db |||||  
Qy 361 GTCTCTGCTTGGACTATCTACATTCGGAAGAAAGATTGTGTACCGTGATCTCAAGTTGGAG 420  
Db |||||  
Qy 776 GTCTCTGCTTGGACTATCTACATTCGGAAGAAAGATTGTGTACCGTGATCTCAAGTTGGAG 835  
Qy 421 AATCTAATGCTGGACAAGATGGCCACATATAAATTTACAGATTTTGACATTTGCAAGAA 480  
Db |||||  
Qy 836 AATCTAATGCTGGACAAGATGGCCACATATAAATTTACAGATTTTGACATTTGCAAGAA 895  
Qy 481 GGGATCAGATGCGAGCCACCATGAAGACATTTCTGTGGCCTCCAGAAATATCTGGCACCA 540  
Db |||||  
Qy 896 GGGATCAGATGCGAGCCACCATGAAGACATTTCTGTGGCCTCCAGAAATATCTGGCACCA 955  
Qy 541 GAGGTGTTGAAGATAATGACTATGGCGAGCAGTAGACTGGTGGGCGCTAGGGGTTGTC 600  
Db |||||  
Qy 956 GAGGTGTTGAAGATAATGACTATGGCGAGCAGTAGACTGGTGGGCGCTAGGGGTTGTC 1015  
Qy 601 ATGTATGAATGATGTGGGAGGTACCTTTCTACACGAGGACCATGAGAACTTTT 660  
Db |||||  
Qy 1016 ATGTATGAATGATGTGGGAGGTACCTTTCTACACGAGGACCATGAGAACTTTT 1075  
Qy 661 GAATTAATTAATGAAGACATTAATAATTTCTCGAACACTCTCTTCAGATGCAAAATCA 720  
Db |||||  
Qy 1076 GAATTAATTAATGAAGACATTAATAATTTCTCGAACACTCTCTTCAGATGCAAAATCA 1135  
Qy 721 TTGCTTTTCAGGGCTCTTGATAAAGATGCAAAATTAACGCTTGTGGAGGACGATGAT 780  
Db |||||  
Qy 1136 TTGCTTTTCAGGGCTCTTGATAAAGATGCAAAATTAACGCTTGTGGAGGACGATGAT 1195  
Qy 781 GCAAAAGAAATATGAGACACAGTTTCTCTCGAGTAACTGCGAAGATGTATATGAT 840  
Db |||||  
Qy 1196 GCAAAAGAAATATGAGACACAGTTTCTCTCGAGTAACTGCGAAGATGTATATGAT 1255  
Qy 841 AAAAAGCTTGACCTCTCTTTTAAACCTCAAGTAACATCTGAGACAGATACCTAGATATTTT 900  
Db |||||  
Qy 1256 AAAAGCTTGACCTCTCTTTTAAACCTCAAGTAACATCTGAGACAGATACCTAGATATTTT 1315  
Qy 901 GATGAAGATTTACAGCTCAGATCTATTAATAACACACCTGAAAAATATGATGAGAT 960  
Db |||||  
Qy 1316 GATGAAGATTTACAGCTCAGATCTATTAATAACACACCTGAAAAATATGATGAGAT 1375  
Qy 961 GGTATGGACTGCATGGAC 978  
Db |||||  
Qy 1376 GGTATGGACTGCATGGAC 1393

RESULT 6  
AAC61592  
ID AAC61592 standard; DNA; 2367 BP.  
XX AC  
XX AAC61592;  
DT 19-FEB-2001 (first entry)  
XX AC  
XX DNA encoding a human kinase B-gamma polypeptide.  
DE XX  
KW Human; protein kinase B gamma; PKB; insulin; insulin growth factor 1;  
KW phosphoinositide 3-kinase; insulin signalling;  
KW pleckstrin homology domain; ss.  
XX XX  
OS Homo sapiens.  
XX XX  
FH Key Location/Qualifiers  
FT CDS 10..1449  
FT /\*tag= a  
FT /product= "kinase B-gamma polypeptide"  
XX XX  
XX WO200058446-A1.  
XX XX

PD 05-OCT-2000.  
XX XX  
PF 23-MAR-2000; 2000WO-SB000571.  
XX XX  
PR 25-MAR-1999; 99SE-00001115.  
XX XX  
PA (PHAA ) PHARMACIA & UPJOHN AB.  
XX XX  
PI Attersand A;  
XX XX  
DR WPI; 2000-647230/62.  
DR P-PSDB; AAB19284.  
XX XX  
PT Novel human protein kinase B gamma polynucleotides and polypeptides  
PT useful as probe or primers in polymerase chain reaction and to raise  
PT antibodies useful in diagnostic assays for detecting polypeptide  
PT expression.  
XX XX  
PS Claim 1; Page 16-19; 27pp; English.  
XX XX  
CC The present sequence encodes a human protein kinase B gamma (PKB)  
CC polypeptide. PKB is activated by insulin or insulin growth factor 1.  
CC Lipid products of phosphoinositide 3-kinase act in insulin signaling by  
CC binding to pleckstrin homology domains of PKB. PKB polynucleotides may be  
CC used as a source of probes and primers. PKB polypeptides are used to  
CC raise antibodies, which are used in diagnostic assays. The polypeptides  
CC are also useful for screening for compounds which affect insulin  
CC signalling pathways  
XX XX  
SQ Sequence 2367 BP; 752 A; 444 C; 514 G; 657 T; 0 U; 0 Other;  
Query Match 100.0%; Score 978; DB 3; Length 2367;  
Best Local Similarity 100.0%; Pred. No. 1.6e-257;  
Matches 978; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 TCTACACCCATCATAAAGAAAGACAATGAATGATTTTGCATCTATTGAAACTACTAGGT 60  
Db 415 TCTACACCCATCATAAAGAAAGACAATGAATGATTTTGCATCTATTGAAACTACTAGGT 474  
Qy 61 AAGGCACATTTGGGAAAGTTATTTGGTTCGAGAGAGGCAAGTGGAAATACTATGCT 120  
Db 475 AAGGCACATTTGGGAAAGTTATTTGGTTCGAGAGAGGCAAGTGGAAATACTATGCT 534  
Qy 121 ATGAAGATTCTGAAGAAAGAAAGTCATTATTGCAAGGATGAAGTGGCACACACTCTAACT 180  
Db 535 ATGAAGATTCTGAAGAAAGAAAGTCATTATTGCAAGGATGAAGTGGCACACACTCTAACT 594  
Qy 181 GAAAGCAGAGTATTAAGAAACACTAGACATCCCTTTTAAACATCCTTTGAAATATTCCTTC 240  
Db 595 GAAAGCAGAGTATTAAGAAACACTAGACATCCCTTTTAAACATCCTTTGAAATATTCCTTC 654  
Qy 241 CAGACAAAGACCGTTTGTGTTTGTGATGGAATATGTTAATGGGCGAGCTGTTTTTC 300  
Db 655 CAGACAAAGACCGTTTGTGTTTGTGATGGAATATGTTAATGGGCGAGCTGTTTTTC 714  
Qy 301 CATTGTGCGAGAGCGGGTGTCTCTCGAGGACCGCACACGTTTCTATGTCGAGAAATT 360  
Db 715 CATTGTGCGAGAGCGGGTGTCTCTCGAGGACCGCACACGTTTCTATGTCGAGAAATT 774  
Qy 361 GTCTCTGCTTGGACTATCTACATTCGGAAGAAAGATTGTGTACCGTGATCTCAAGTTGGAG 420  
Db 775 GTCTCTGCTTGGACTATCTACATTCGGAAGAAAGATTGTGTACCGTGATCTCAAGTTGGAG 834  
Qy 421 AATCTAATGCTGGACAAGATGGCCACATATAAATTTACAGATTTTGACATTTGCAAGAA 480  
Db 835 AATCTAATGCTGGACAAGATGGCCACATATAAATTTACAGATTTTGACATTTGCAAGAA 894  
Qy 481 GGGATCAGATGCGAGCCACCATGAAGACATTTCTGTGGCCTCCAGAAATATCTGGCACCA 540  
Db 895 GGGATCAGATGCGAGCCACCATGAAGACATTTCTGTGGCCTCCAGAAATATCTGGCACCA 954  
Qy 541 GAGGTGTTGAAGATAATGACTATGGCGAGCAGTAGACTGGTGGGCGCTAGGGGTTGTC 600  
Db |||||

Db 955 GAGGTGTTAGAAATAATGACTATATGCGGAGCAGTAGACTGTGTGGGCTTAGGGTTGTC 1014  
QY 601 ATGTATGAAATGATGTGGAGGTTACTTTCTCAACCCAGGACCATGAGAAACTTTT 660  
Db 1015 ATGTATGAAATGATGTGGAGGTTACTTTCTCAACCCAGGACCATGAGAAACTTTT 1074  
QY 661 GAATTAATATTAATGGAACACATTAATTTCTCGAACAACCTCTCTCAGATGCAAAATCA 720  
Db 1075 GAATTAATATTAATGGAACACATTAATTTCTCGAACAACCTCTCTCAGATGCAAAATCA 1134  
QY 721 TTGCTTTTCAGGCTCTTGATAAAGGATCCAAATAAACCGCTTTGGTGGAGCACGATGAT 780  
Db 1135 TTGCTTTTCAGGCTCTTGATAAAGGATCCAAATAAACCGCTTTGGTGGAGCACGATGAT 1194  
QY 781 GCAAAAGAAATATGAGACACAGTTTCTCTCTGAGATGAATCTGTCAGATGATATGAT 840  
Db 1195 GCAAAAGAAATATGAGACACAGTTTCTCTCTGAGATGAATCTGTCAGATGATATGAT 1254  
QY 841 AAAAGCTGTGACCTCTTTTAAACCTCAAGTAACATCTGAGACAGACTAGATATTTT 900  
Db 1255 AAAAGCTGTGACCTCTTTTAAACCTCAAGTAACATCTGAGACAGACTAGATATTTT 1314  
QY 901 GATGAAGAAATTTACAGCTCAGACTTACAAATAACACACCTGAAATAATATGATGAGAT 960  
Db 1315 GATGAAGAAATTTACAGCTCAGACTTACAAATAACACACCTGAAATAATATGATGAGAT 1374  
QY 961 GGTATGGACTGCATGGAC 978  
Db 1375 GGTATGGACTGCATGGAC 1392

## RESULT 7

ADC26888  
ID ADC26888 standard; DNA; 2811 BP.  
XX AC ADC26888;  
XX 18-DEC-2003 (first entry)  
XX DE DNA encoding human Akt3.  
KW ds; gene; Akt; human; apoptosis; myocardial infarction;  
KW hyperproliferative disease; cancer; rheumatoid arthritis;  
KW inflammatory bowel disease; osteoarthritis; leiomyoma; adenoma; lipoma;  
KW haemangioma; fibroma; vascular occlusion; restenosis; atherosclerosis;  
KW pre-neoplastic lesion; adenomatous hyperplasia;  
KW prostatic intraepithelial neoplasia; carcinoma in situ;  
KW oral hairy leukoplakia; psoriasis.  
XX OS Homo sapiens.  
XX PN US2003144204-A1.  
XX 31-JUL-2003.  
XX PD 19-DEC-2002; 2002US-00324985.  
XX PF 19-DEC-2001; 2001US-0342155P.  
XX PR (BAYU ) BAYLOR COLLEGE MEDICINE.  
XX PA Spencer D;  
XX PI WPI; 2003-720709/68.  
XX DR New expression vector for modulating apoptosis or for treating myocardial  
PT infarction or cancer, comprises an inducible chimeric protein that  
PT comprises a mutant Akt polypeptide fused to a ligand-binding domain.  
XX PS Disclosure; SEQ ID NO 4; 38pp; English.  
XX CC The invention relates to an expression vector comprising an inducible  
chimeric protein which comprises a mutant Akt polypeptide fused to a

CC ligand-binding domain. The composition and methods are useful in  
CC modulating apoptosis or in treating myocardial infarction or  
CC hyperproliferative diseases such as cancer, rheumatoid arthritis,  
CC inflammatory bowel disease, osteoarthritis, leiomyomas, adenomas,  
CC lipomas, haemangiomas, fibromas, vascular occlusion, restenosis,  
CC atherosclerosis, pre-neoplastic lesions (e.g. adenomatous hyperplasia or  
CC prostatic intraepithelial neoplasia), carcinoma in situ, oral hairy  
CC leukoplakia or psoriasis. The present sequence represents DNA encoding  
CC human Akt3.  
XX  
SQ Sequence 2811 BP; 905 A; 506 C; 582 G; 818 T; 0 U; 0 Other;  
Query Match 100.0%; Score 978; DB 10; Length 2811;  
Best Local Similarity 100.0%; Pred. No. 1.7e-257;  
Matches 978; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TCTCAACCCCATCAATAAAGAAAGCAATGAATGATTTTGACTATTTGAAACTACTAGT 60  
Db 406 TCTCAACCCCATCAATAAAGAAAGCAATGAATGATTTTGACTATTTGAAACTACTAGT 465  
QY 61 AAAGCACTTTTGGGAAAGTTATTTTGGTTCGAGAGAGGCAAGTGGAAAACTATATGT 120  
Db 466 AAAGCACTTTTGGGAAAGTTATTTTGGTTCGAGAGAGGCAAGTGGAAAACTATATGT 525  
QY 121 ATGAAGATCTGAAGAAAGAAAGTCAATTTTGCAGAGAGGATGAAGTGGCACACACTCTA 180  
Db 526 ATGAAGATCTGAAGAAAGAAAGTCAATTTTGCAGAGAGGATGAAGTGGCACACACTCTA 585  
QY 181 GAAAGCAGATGTTAAAGAAACACTAGACATCCCTTTTAAACATCTTGAATATATTCCTTC 240  
Db 586 GAAAGCAGATGTTAAAGAAACACTAGACATCCCTTTTAAACATCTTGAATATATTCCTTC 645  
QY 241 CAGACAAAGACCGTTTGTGTTTGTGATGGAATATGTTAATGGGGGCGAGCTGTTTTTC 300  
Db 646 CAGACAAAGACCGTTTGTGTTTGTGATGGAATATGTTAATGGGGGCGAGCTGTTTTTC 705  
QY 301 CATTTGTCGAGAGCGGGTGTCTCTGAGGACCCGACACACGTTTCTATGTCGACAGAAAT 360  
Db 706 CATTTGTCGAGAGCGGGTGTCTCTGAGGACCCGACACACGTTTCTATGTCGACAGAAAT 765  
QY 361 GTCTCTGCTTGGACTATCTACATTCGGAAGATTTGTACCGTGATCTCAAGTTGGAG 420  
Db 766 GTCTCTGCTTGGACTATCTACATTCGGAAGATTTGTACCGTGATCTCAAGTTGGAG 825  
QY 421 AATCTAATGCTGGCAAAAGATGGCCACATAAATAATACAGATTTTGGACTTTGCAAGAA 480  
Db 826 AATCTAATGCTGGCAAAAGATGGCCACATAAATAATACAGATTTTGGACTTTGCAAGAA 885  
QY 481 GGGATCAGATGCGAGCCACCATGAAGACATCTCTGGCACTCCAGAAATATCTGGCACCA 540  
Db 886 GGGATCAGATGCGAGCCACCATGAAGACATCTCTGGCACTCCAGAAATATCTGGCACCA 945  
QY 541 GAGGTGTTAGAAAGATAATGACTATATGCGGAGCAGTAGACTGTGTGGGCTTAGGGTTGTC 600  
Db 946 GAGGTGTTAGAAAGATAATGACTATATGCGGAGCAGTAGACTGTGTGGGCTTAGGGTTGTC 1005  
QY 601 ATGTATGAAATGATGTGTGGAGGTTTACCTTTCTCAACCCAGGACCATGAGAAACTTTT 660  
Db 1006 ATGTATGAAATGATGTGTGGAGGTTTACCTTTCTCAACCCAGGACCATGAGAAACTTTT 1065  
QY 661 GAATTAATATTAATGGAAGACATTAATTTCTCGAACAACCTCTCTCAGATGCAAAATCA 720  
Db 1066 GAATTAATATTAATGGAAGACATTAATTTCTCGAACAACCTCTCTCAGATGCAAAATCA 1125  
QY 721 TTGCTTTTCAGGCTCTTGATAAAGGATCCAAATAAACCGCTTTGGTGGAGCACGATGAT 780  
Db 1126 TTGCTTTTCAGGCTCTTGATAAAGGATCCAAATAAACCGCTTTGGTGGAGCACGATGAT 1185  
QY 781 GCAAAAGAAATATGAGACACAGTTTCTCTCTGAGATGAATCTGTCAGATGATATGAT 840  
Db 1186 GCAAAAGAAATATGAGACACAGTTTCTCTCTGAGATGAATCTGTCAGATGATATGAT 1245  
QY 841 AAAAGCTGTGACCTCTTTTAAACCTCAAGTAACATCTGAGACAGACTAGATATTTT 900

Db 1246 AAAAGCTGTACCTCTTTTAAACCTCAAGTAACATCTGAGACAGATAGATATTTT 1305  
Qy 901 GATCAAGAAATTTACAGCTTCAGACTATTACAAATAACACACCTGAAAATATGATGAGGAT 960  
Db 1306 GATCAAGAAATTTACAGCTTCAGACTATTACAAATAACACACCTGAAAATATGATGAGGAT 1365  
Qy 961 GGTATGGACTCATGGAC 978  
Db 1366 GGTATGGACTCATGGAC 1383  
RESULT 8  
ID ADQ88265  
XX ADQ88265 standard; DNA; 2811 BP.  
XX AC ADQ88265;  
XX DT 21-OCT-2004 (first entry)  
XX DE Human 14180 DNA encodes a rac gamma Ser/Thr protein kinase RAC-PK-gamma.  
XX KW human; gene; ds; cardiovascular disorder; thrombotic disorder;  
XX KW differential expression; gene therapy; aberrant vascularisation;  
XX KW atherosclerosis; thrombosis; coronary artery disease; hyperlipidaemia;  
XX KW dyslipidaemia; high blood pressure; heart failure; cardiant;  
XX KW thrombolytic; anticoagulant; antilipaeamic; hypotensive; cardiant;  
XX KW rac gamma Ser/Thr protein kinase; RAC-PK-gamma.  
XX OS Homo sapiens.  
XX FN WO2004063340-A2.  
XX PD 29-JUL-2004.  
XX FF 13-JAN-2004; 2004WO-US000393.  
XX PR 13-JAN-2003; 2003US-0439683P.  
XX PR 05-FEB-2003; 2003US-0445216P.  
XX PR 18-FEB-2003; 2003US-0448036P.  
XX PR 12-MAR-2003; 2003US-0454189P.  
XX PR 25-MAR-2003; 2003US-0457541P.  
XX PR -29-APR-2003; 2003US-0466411P.  
XX PR 08-MAY-2003; 2003US-0469041P.  
XX PR 10-JUN-2003; 2003US-0477414P.  
XX PR 13-JUN-2003; 2003US-0478560P.  
XX PR 24-JUL-2003; 2003US-0489772P.  
XX PR 28-JUL-2003; 2003US-0490660P.  
XX PR 03-SEP-2003; 2003US-0499838P.  
XX PR 22-SEP-2003; 2003US-0504786P.  
XX PR 24-SEP-2003; 2003US-0505570P.  
XX PR 17-OCT-2003; 2003US-0512418P.  
XX PR 27-OCT-2003; 2003US-0514660P.  
XX PA (MILL-) MILLENNIUM PHARM INC.  
XX PI Stagliano NE, Healy A, Acton SL, Galvin KM, Donoghue MA;  
XX PI Rogrue-Way A, Tomlinson JE;  
XX DR WPI; 2004-553729/53.  
XX DR P-PSDB; ADQ88266.  
XX PT Identifying a compound for treating a cardiovascular or thrombotic  
XX disorder by combining a compound to be tested with e.g., a 9380, 9462,  
XX 8701 or 2419 polypeptide or with a host cell expressing the polypeptide  
XX and detecting the binding.  
XX PS Claim 1; SEQ ID NO 107; 512pp; English.  
XX CC This invention relates to a novel compound that is capable of treating a  
XX cardiovascular or thrombotic disorder. Specifically, it refers to the  
XX identification of nucleic acid molecules, and the encoded proteins  
XX thereof, which are differentially expressed in cardiovascular disease

CC states relative to their normal expression in non-diseased tissue. The  
CC present invention describes test compounds (i.e. small molecules,  
CC peptides or antibodies) that can bind to and modulate the activity of  
CC these differentially expressed membrane-bound polypeptides, where binding  
CC is detected by a competition binding assay, immuncassay or yeast two-  
CC hybrid assay. Accordingly, pharmaceutical compositions can be developed  
CC and used via gene therapy to treat aberrant vascularisation,  
CC atherosclerosis, thrombosis, coronary artery disease, hyperlipidaemia,  
CC dyslipidaemia, high blood pressure or heart failure. As such, they  
CC exhibit cardiant, thrombolytic, anticoagulant, antilipaeamic, hypotensive  
CC and cardiant activities. This polynucleotide sequence is a human DNA  
CC molecule that is differentially expressed in a patient with a  
CC cardiovascular disorder, given in an exemplification of the invention.  
XX SQ Sequence 2811 BP; 905 A; 506 C; 582 G; 818 T; 0 U; 0 Other;  
Query Match 100.0%; Score 978; DB 13; Length 2811;  
Best Local Similarity 100.0%; Pred. No. 1.7e-257;  
Matches 978; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 TCTACRACCCATCATATAAAGAGACAAATGAATGATTTTGACTATTTTGAAACTACTAGGT 60  
Db 406 TCTACRACCCATCATATAAAGAGACAAATGAATGATTTTGACTATTTTGAAACTACTAGGT 465  
Qy 61 AAAGGCACCTTTTGGGAAAGTATTTTGGTTGCGAGAGAGCAAGTGGAAAATATCTATGCT 120  
Db 466 AAAGGCACCTTTTGGGAAAGTATTTTGGTTGCGAGAGAGCAAGTGGAAAATATCTATGCT 525  
Qy 121 ATGNAGATCTGAAGAAGAAGTCAATTTATGCAAAAGATGAAGTGGGCACACACTTAACT 180  
Db 526 ATGAAGATCTGAAGAAGAAGTCAATTTATGCAAAAGATGAAGTGGGCACACACTTAACT 585  
Qy 181 GAAAGCAGAGTATTAAAGAAACACATAGACATCCCTTTTAAACATCCTTTGAAATATTCCTTC 240  
Db 586 GAAAGCAGAGTATTAAAGAAACACATAGACATCCCTTTTAAACATCCTTTGAAATATTCCTTC 645  
Qy 241 CAGACAAAACACCGTTTGTGTTTGTGATGGAATATGTTAATGGGGCGAGCTGTTTTTC 300  
Db 646 CAGACAAAACACCGTTTGTGTTTGTGATGGAATATGTTAATGGGGCGAGCTGTTTTTC 705  
Qy 301 CATTTGTCGAGAGACGGGTGTTCTCTGAGGACCGCACACGTTTCTATGGTGCAAGAAAT 360  
Db 706 CATTTGTCGAGAGACGGGTGTTCTCTGAGGACCGCACACGTTTCTATGGTGCAAGAAAT 765  
Qy 361 GTCTCTGCTTGGACTATCTACATTCGCGAAAGATTTGTACCGTGATCTCAAGTTGGAG 420  
Db 766 GTCTCTGCTTGGACTATCTACATTCGCGAAAGATTTGTACCGTGATCTCAAGTTGGAG 825  
Qy 421 AATCTAATGTCGACAAAGATGGCCACATAAAAATTAACAGATTTGGACTTTGCAAGAA 480  
Db 826 AATCTAATGTCGACAAAGATGGCCACATAAAAATTAACAGATTTGGACTTTGCAAGAA 885  
Qy 481 GGGATCACAGATGCGACCAACATGAAGACATTTGTGGCACTCCAGATATATCTGGCACA 540  
Db 886 GGGATCACAGATGCGACCAACATGAAGACATTTGTGGCACTCCAGATATATCTGGCACA 945  
Qy 541 GAGGTGTTAGAAGATAATGACTATGGCCGAGCAGTAGACTGTGGGGCTTAGGGGTTGTC 600  
Db 946 GAGGTGTTAGAAGATAATGACTATGGCCGAGCAGTAGACTGTGGGGCTTAGGGGTTGTC 1005  
Qy 601 ATGATGAAATGATGTGCGAGGTTTACCTTTTCAACACAGGACCATGAGAAACTTTTT 660  
Db 1006 ATGATGAAATGATGTGCGAGGTTTACCTTTTCAACACAGGACCATGAGAAACTTTTT 1065  
Qy 661 GAATTAATATTAATGGAAGACATTAATTTTCTCGAACACTCTCTTCAGATGCAAAATCA 720  
Db 1066 GAATTAATATTAATGGAAGACATTAATTTTCTCGAACACTCTCTTCAGATGCAAAATCA 1125  
Qy 721 TTGCTTTTCAAGGCTCTTGATAAAGATCCAAATAAACGCCCTTGGTGAGGACCATGAT 780  
Db 1126 TTGCTTTTCAAGGCTCTTGATAAAGATCCAAATAAACGCCCTTGGTGAGGACCATGAT 1185  
Qy 781 GCAAAAGAAATATGAGACACAGTTTCTTCTCTGGAGTAAACTGGCAAGATGTATATGAT 840



Db	1186	GCAAAAGAAATTATGAGACACAGTTCTTCTCTGGAGTAAACTGCGAAGATGTATATGAT	1245
Qy	841	AAAAAGCTTGTACCTCCCTTTTAAACCTCAAGTAAACATCTGAGACAGATACCTAGATATTTT	900
Db	1246	AAAAAGCTTGTACCTCCCTTTTAAACCTCAAGTAAACATCTGAGACAGATACCTAGATATTTT	1305
Qy	901	GATGAAGAATTACAGCTCAGACTATTACAAATAACACACCTGAAAAATATGATGAGAT	960
Db	1306	GATGAAGAATTACAGCTCAGACTATTACAAATAACACACCTGAAAAATATGATGAGAT	1365
Qy	961	GGTATGAGCTGCATGGAC	978
Db	1366	GGTATGAGCTGCATGGAC	1383
RESULT	9		
ID	AAC77341		
ID	AAC77341	standard; cDNA; 3285 BP.	
XX	AAC77341;		
XX	XX		
DT	08-FEB-2001	(first entry)	
DE	Human ORFX ORF2896	polynucleotide sequence SEQ ID NO:5791.	
XX	Human; open reading frame; ORFX; detection; cytostatic; hepatotropic;		
XX	vulnery; antipsoriatic; antiparkinsonian; nootropic; neuroprotective;		
KW	anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant;		
KW	immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;		
KW	hypotensive; dermatological; immunosuppressive; antiinflammatory;		
KW	antiviral; antibacterial; antifungal; antirheumatic; antithyroid;		
KW	antianemic; gene therapy; cancer; proliferative disorder; hypertension;		
KW	neurodegenerative disorder; osteoarthritis; graft vs host disease;		
KW	cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;		
KW	cholesterol ester storage; systemic lupus erythematosus; infection;		
KW	severe combined immunodeficiency; malaria; autoimmune disorder; asthma;		
KW	allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;		
KW	bone damage; cartilage damage; antiinflammatory disease; coagulation;		
KW	thrombosis; contraceptive; ss.		
OS	Homo sapiens.		
XX	XX		
PN	WO200058473-A2.		
XX	XX		
PD	05-OCT-2000.		
XX	XX		
PF	31-MAR-2000; 2000WO-US008621.		
XX	XX		
PR	31-MAR-1999; 99US-0127607P.		
PR	02-APR-1999; 99US-0127636P.		
PR	05-APR-1999; 99US-0127728P.		
PR	30-MAR-2000; 2000US-00540763.		
XX	XX		
PA	(CURA-) CURAGEN CORP.		
XX	XX		
PI	Shimkets RA, Leach M;		
XX	XX		
DR	WPI; 2000-602362/57.		
DR	P-PSD; AAB43132.		
XX	XX		
PT	Novel nucleic acids and peptides derived from open reading frame X,		
PT	useful for treating e.g. cancers, proliferative disorders,		
PT	neurodegenerative disorders and cardiovascular disease.		
XX	XX		
PS	Claim 5; Page 4956-4958; 5507pp; English.		
XX	XX		
CC	AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397,		
CC	which represent the human ORFX open reading frames 1 to 3161. The ORFX		
CC	sequences have activities such as: cytostatic; hepatotropic; vulnery;		
CC	antipsoriatic; antiparkinsonian; nootropic; neuroprotective; osteopathic;		
CC	anticonvulsant; antiarthritic; immunosuppressant; immunostimulant;		
CC	cardiant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive;		

Qy 781 GCAAAAGAAATATGAGACACAGTTTCTCTCTGGAGTAAACTGGCAAGATGTATATGAT 840  
Db 1660 GCAAAAGAAATATGAGACACAGTTTCTCTCTGGAGTAAACTGGCAAGATGTATATGAT 1719  
Qy 841 AAAAGCTTGTACCTCTTTTAAACCTCAAGTAACTCTGAGACAGATAGTATATTTT 900  
Db 1720 AAAAGCTTGTACCTCTTTTAAACCTCAAGTAACTCTGAGACAGATAGTATATTTT 1779  
Qy 901 GATGAAGAATTTACAGCTCAGACTATTACAAATAACACCACCTGAAAAATATGATGAGAT 960  
Db 1780 GATGAAGAATTTACAGCTCAGACTATTACAAATAACACCACCTGAAAAATATGATGAGAT 1839  
Qy 961 GGTATGGAATGCATGGAC 978  
Db 1840 GGTATGGAATGCATGGAC 1857

RESULT 10

AAA96637

ID AAA96637 standard; DNA; 1570 BP.

XX

AC AAA96637;

DT 08-FEB-2001 (first entry)

XX DNA encoding a human Akt3 polypeptide.

XX Human; Akt3; apoptotic cell death; apoptotic stimulating kinase 1; ASK1;  
KW hypoxia; apoptosis; necrosis; myocardial infarction; ischemia;  
KW reperfusion injury; myocardial ischemia reperfusion injury; stroke;  
KW liver damage; renal failure; organ transplantation; coronary artery; ss.

XX Homo sapiens.

XX

FH Key Location/Qualifiers  
CDS 126..1523

FT /\*tag= a

FT /product= "Akt3"

XX

PN WO200056866-A2.

XX

PD 28-SEP-2000.

XX

PF 14-MAR-2000; 2000WO-US006574.

XX

PR 19-MAR-1999; 99US-0125108P.

XX

PA (AVET ) AVENTIS PHARM PROD INC.

XX Guo K, Pagnoni MF, Clark KL, Ivaehchenko YD;

XX WPI; 2000-638260/61.

DR P-PSDB; AAB19011.

XX

PT Novel AKT3 nucleic acid and proteins capable of preventing apoptotic cell  
death induced by apoptosis stimulating kinase 1 useful for treating  
myocardial infarction or ischemia reperfusion injury.

XX Claim 3; Page 62-64; 73pp; English.

XX

CC The present sequence encodes a human Akt3 protein. Expression of Akt3  
prevents apoptotic cell death induced by apoptotic stimulating kinase 1  
(ASK1). The Akt3 polypeptide is useful for inhibiting cell death,  
preferably in a cardiac myocyte, resulting from hypoxia, apoptosis or  
necrosis in a patient suffering from myocardial infarction or ischemia  
reperfusion injury. The polypeptide is also useful for treating  
myocardial infarction or ischemia reperfusion injury, where the  
reperfusion injury is myocardial ischemia reperfusion injury or is  
associated with stroke, liver damage, renal failure, organ  
transplantation or coronary artery by pass grafting

XX Sequence 1570 BP; 553 A; 267 C; 358 G; 392 T; 0 U; 0 Other;

SQ

Query Match 97.1%; Score 949.8; DB 3; Length 1570;  
Best Local Similarity 99.8%; Pred. No. 7.5e-250;  
Matches 951; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Qy 1 TCTACAAACCATCATAAAGAAAGACAAATGAATGATTTTGACTATTTGAAACTACTAGGT 60  
Db 531 TCTACAAACCATCATAAAGAAAGACAAATGAATGATTTTGACTATTTGAAACTACTAGGT 590  
Qy 61 AAAGGCACTTTTGGGAAAGTTATTTTGGTTTCGAGAGAGGCAAGTGGAAATATCTATGCT 120  
Db 591 AAAGGCACTTTTGGGAAAGTTATTTTGGTTTCGAGAGAGGCAAGTGGAAATATCTATGCT 650  
Qy 121 ATGAAGATTCTGAAGAAAGAGTCAATTTATTCGAAAGGATGAAGTGGCACACACTCTAACT 180  
Db 651 ATGAAGATTCTGAAGAAAGAGTCAATTTATTTGAAAGGATGAAGTGGCACACACTCTAACT 710  
Qy 181 GAAAGCAGAGTATTAAGAAACACATAGACATCCCTTTTAAACATCCTTGAATATATCTTTC 240  
Db 711 GAAAGCAGAGTATTAAGAAACACATAGACATCCCTTTTAAACATCCTTGAATATATCTTTC 770  
Qy 241 CAGACAAAAGACCGTTTGTGTTTGTGATGGAATATGTTAATGGGGCGAGCTGTTTTTC 300  
Db 771 CAGACAAAAGACCGTTTGTGTTTGTGATGGAATATGTTAATGGGGCGAGCTGTTTTTC 830  
Qy 301 CATTTGTGAGAGAGCGGGTGTCTCTGAGGACCGCACACAGTTTCTATGTCGAGAAATTT 360  
Db 831 CATTTGTGAGAGAGCGGGTGTCTCTGAGGACCGCACACAGTTTCTATGTCGAGAAATTT 890  
Qy 361 GTCTCTGCTTGGACTATCTACATTCGGAAAGATTTGTACCGTGATCTCAAGTTGGAG 420  
Db 891 GTCTCTGCTTGGACTATCTACATTCGGAAAGATTTGTACCGTGATCTCAAGTTGGAG 950  
Qy 421 AATCTAATGCTGGCAAAAGATGGCCACATAAATTTACAGATTTTGACATTTTGCAAGAA 480  
Db 951 AATCTAATGCTGGCAAAAGATGGCCACATAAATTTACAGATTTTGACATTTTGCAAGAA 1010  
Qy 481 GGGATCACAGATGCAGCCACCATGAAGACATTTCTGTGGCACTCCAGAAATATCTGGCACA 540  
Db 1011 GGGATCACAGATGCAGCCACCATGAAGACATTTCTGTGGCACTCCAGAAATATCTGGCACA 1070  
Qy 541 GAGGTGTTAAGAAATATGACTATGGCCGAGCAGTAGACTGGTGGGGCCTAGGGGTGTC 600  
Db 1071 GAGGTGTTAAGAAATATGACTATGGCCGAGCAGTAGACTGGTGGGGCCTAGGGGTGTC 1130  
Qy 601 ATGTATGAAATGATGTGGGAGTTTACCTTTCTACAAACGAGGACCATGAGAAATCTTTT 660  
Db 1131 ATGTATGAAATGATGTGGGAGTTTACCTTTCTACAAACGAGGACCATGAGAAATCTTTT 1190  
Qy 661 GAATTAATATTAATGGAAGACATTTAAATTTCTCGAACACTCTCTTCAGATGCAAAATCA 720  
Db 1191 GAATTAATATTAATGGAAGACATTTAAATTTCTCGAACACTCTCTTCAGATGCAAAATCA 1250  
Qy 721 TTGCTTTTCAGGGCTCTTGATAAAGGATCCAAATAAACGCCCTTGGTGGAGGACGATGAT 780  
Db 1251 TTGCTTTTCAGGGCTCTTGATAAAGGATCCAAATAAACGCCCTTGGTGGAGGACGATGAT 1310  
Qy 781 GCAAAAGAAATTTAGACACACAGTTTCTCTCTGGAGTAACTGGCAAGATGTATATGAT 840  
Db 1311 GCAAAAGAAATTTAGACACACAGTTTCTCTCTGGAGTAACTGGCAAGATGTATATGAT 1370  
Qy 841 AAAAAGCTGTACCTCTCTTTTAAACCTCAAGTAACTCTGAGACAGATAGTATATTTT 900  
Db 1371 AAAAAGCTGTACCTCTCTTTTAAACCTCAAGTAACTCTGAGACAGATAGTATATTTT 1430  
Qy 901 GATGAAGAATTTACAGCTCAGACTATTACAAATAACACACCTGAAAAATATGA 953  
Db 1431 GATGAAGAATTTACAGCTCAGACTATTACAAATAACACACCTGAAAAATATGA 1483

RESULT 11

AAH79025

ID AAH79025 standard; cDNA; 1570 BP.

XX



XX DE Human serine/threonine protein kinase Akt3 cDNA.  
XX AKT3; human; protein kinase; vascular endothelial growth factor; VEGF;  
KW inducer; ischaemia; cardiomyopathy; angiogenesis; tumour; gene therapy;  
KW ss.  
XX OS Homo sapiens.  
XX FH Key Location/Qualifiers  
FT CDS 126..1523  
FT /\*tag= a  
XX PN WO200077190-A2.  
XX PD 21-DEC-2000.  
XX PF 01-JUN-2000; 2000WO-US015098.  
XX PR 11-JUN-1999; 99US-0138724P.  
XX PR 03-NOV-1999; 99GB-00026058.  
XX PA (AVET ) AVENTIS PHARM PROD INC.  
XX FI Guo K, Ivashchenko Y, Clark K;  
XX DR WPI; 2001-025336/03.  
XX DR P-PSDB; AAB19996.  
XX PT Inducing expression of vascular endothelial growth factor, useful for  
PT treating an ischemic condition, e.g. cerebrovascular ischemia, renal  
PT ischemia or pulmonary ischemia, comprises administering a  
PT serine/threonine protein kinase Akt protein.  
XX  
XX Example 1; Page 55-58; 67pp; English.  
XX  
XX The present sequence is that of cDNA coding for human Akt3 (see  
CC AAB19996), a novel Akt isoform. Akt3 is a serine/threonine protein kinase  
CC capable of inducing vascular endothelial growth factor (VEGF) expression.  
CC The sequence was deduced from 2 cDNA clones isolated from a human heart  
CC cDNA library using a human Akt3 partial clone as probe. Akt3 is shorter  
CC than Akt1 (see AAB1997) and Akt2 (see AAB19998) and there is no  
CC significant homology between Akt3 and Akt1 or Akt2 at the C-terminus of  
CC the molecules. A claimed method of inducing expression of VEGF in a cell  
CC involves administering Akt1, Akt2 or Akt3, or a nucleic acid encoding  
CC such a protein. The cell is preferably from a patient suffering from an  
CC ischaemic condition, especially cerebrovascular, renal, pulmonary, limb  
CC or myocardial ischaemia, or ischaemic, idiopathic or hypertrophic  
CC cardiomyopathy. The result is beneficial collateral blood vessel  
CC formation. A claimed method of inhibiting angiogenesis in a patient  
CC suffering from a tumour, comprises inhibiting the level of Akt activity  
CC in the patient, thereby inhibiting production of VEGF. The method  
CC comprises introducing an Akt antisense nucleic acid, an intracellular  
CC binding protein (e.g. a scFv) that specifically binds the Akt protein, or  
CC a nucleic acid encoding a dominant negative form of an Akt  
XX  
SQ Sequence 1570 BP; 553 A; 267 C; 358 G; 392 T; 0 U; 0 Other;

Query March 97.1%; Score 949.8; DB 4; Length 1570;  
Best Local Similarity 99.8%; Pred. No. 7.5e-250;  
Matches 951; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TCTACACCCCATATAAGAAAGACATGATGATTTTGACTATTGTGAACACTACTAGGT 60  
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Qy 531 TCTACACCCCATATAAGAAAGACATGATGATTTTGACTATTGTGAACACTACTAGGT 590  
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Qy 61 AAAGGCACTTTTGGGAAGTTATTTTGGTTCCAGAGAGGCAAGTGGAAATACTATGCT 120  
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Qy 591 AAAGGCACTTTTGGGAAGTTATTTTGGTTCCAGAGAGGCAAGTGGAAATACTATGCT 650  
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Qy 121 ATGAAGATCTTGAGAGAGAGTATTTATTCGAAGGATGAAGTGGCACACACTCTAACT 180  
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Qy 651 ATGAAGATCTTGAGAGAGAGTATTTATTCGAAGGATGAAGTGGCACACACTCTAACT 710  
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy 181 GAAAGCAGAGTATTAAAGAAACACATAGACATCCCTTTTAAACATCCTTTGAAATATTCCTTC 240  
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Qy 711 GAAAGCAGAGTATTAAAGAAACACATAGACATCCCTTTTAAACATCCTTTGAAATATTCCTTC 770  
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Qy 241 CAGACAAAAGACCGTTTGTGTTTGTGATGGAATATGTTAATGGGGCGAGCTGTTTTTC 300  
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Qy 301 CATTGTGCGAGAGACGGGTGTTCTCTGAGGACCGCACACGTTTCTATGGTGCAGAAATT 360  
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Qy 831 CATTGTGCGAGAGACGGGTGTTCTCTGAGGACCGCACACGTTTCTATGGTGCAGAAATT 890  
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Qy 361 GTCTCTGCTTGGACTATCTACATTCGGGAAAGATTGTGTACCGTGTCTCAAGTTGGAG 420  
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Qy 891 GTCTCTGCTTGGACTATCTACATTCGGGAAAGATTGTGTACCGTGTCTCAAGTTGGAG 950  
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Qy 421 AATCTAATGCTGGACAAAAGATGGCCACATATAAAATTAACAGATTTTGGACTTTGCAAGAA 480  
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Qy 951 AATCTAATGCTGGACAAAAGATGGCCACATATAAAATTAACAGATTTTGGACTTTGCAAGAA 1010  
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Qy 481 GGGATCACAGATGCAGCCACCATGAAGACATTTCTGTGGCACTCCAGATATCTGGCACCA 540  
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Qy 1011 GGGATCACAGATGCAGCCACCATGAAGACATTTCTGTGGCACTCCAGATATCTGGCACCA 1070  
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Qy 541 GAGGTGTTAGAAGATAATGACTATGGCCGAGCAGTAGACTGGTGGGCGCTAGGGGTTGTC 600  
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Qy 1071 GAGGTGTTAGAAGATAATGACTATGGCCGAGCAGTAGACTGGTGGGCGCTAGGGGTTGTC 1130  
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Qy 601 ATGTATGAATGATGTGGAGGTTACCTTTCTACAAACGAGGACCATGAGAAACTTTTT 660  
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Qy 1131 ATGTATGAATGATGTGGAGGTTACCTTTCTACAAACGAGGACCATGAGAAACTTTTT 1190  
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Qy 661 GAATTAATATTAATGGAAGACATTAATTTCCCTCGAACACTCTCTTCAGATGCAAAATCA 720  
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Qy 1191 GAATTAATATTAATGGAAGACATTAATTTCCCTCGAACACTCTCTTCAGATGCAAAATCA 1250  
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Qy 721 TTGCTTTTCAGGGCTCTTGATAAAGGATCCAAATAAAGCGCTTGGTGAGGACCAAGATGAT 780  
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Qy 1251 TTGCTTTTCAGGGCTCTTGATAAAGGATCCAAATAAAGCGCTTGGTGAGGACCAAGATGAT 1310  
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Qy 781 GCAAAAGAAATATGAGACACAGTTTCTTCTGGAGTAACTGCGCAAGATGTATATGAT 840  
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Qy 1311 GCAAAAGAAATATGAGACACAGTTTCTTCTCGAGTAACTGCGCAAGATGTATATGAT 1370  
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Qy 841 AAAAGGCTTCTACTCTCTTTTAAACCTCAAGTAACTCTGAGACAGATCTAGATATTTT 900  
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Qy 1371 AAAAGGCTTCTACTCTCTTTTAAACCTCAAGTAACTCTGAGACAGATCTAGATATTTT 1430  
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Qy 901 GATGAAGAAATTTACAGCTCAGACTATTACAAATAACACACCTGAAAAATATGA 953  
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Qy 1431 GATGAAGAAATTTACAGCTCAGACTATTACAAATAACACACCTGAAAAATATGA 1483  
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
RESULT 13  
ADG85244  
ID ADG85244 standard; DNA; 1570 BP.  
XX AC ADG85244;  
XX DT 25-MAR-2004 (first entry)  
XX OS Human Chrysosporium associated DNA.  
XX DS ds; gene; beta-glucosidic bond; beta-xylosidic bond; human.  
XX OS Homo sapiens.  
XX FH Key Location/Qualifiers  
FT CDS 126..1523  
FT /\*tag= a  
FT /product= "Chrysosporium associated protein"  
XX

PN	US20040021136-A1.	
XX		
PD	01-JAN-2004.	
XX		
PF	21-MAR-2003; 2003US-00394568.	
XX		
PR	06-OCT-1998; 98WO-BP006496.	
PR	06-OCT-1999; 99WO-NL000618.	
PR	13-APR-2000; 2000US-00548938.	
XX		
PA	(EMAL/) EMALFARB M A.	
PA	(BURL/) BURLINGAME R P.	
PA	(OLSO/) OLSON P T.	
PA	(SINI/) SINITSYN A P.	
PA	(PARR/) PARRICHE M.	
PA	(BOUS/) BOUSSON J C.	
PA	(PYNN/) PYNNONEN C M.	
PA	(PUNT/) PUNT P J.	
PA	(VZEI/) VAN ZEIJL C M J.	
XX		
PI	Emalfarb MA, Burlingame RP, Olson PT, Sinitsyn AP, Parriche M;	
PI	Bousson JC, Pynnnonen CM, Punt PJ, Van Zeijl CMJ;	
XX		
DR	WPI; 2004-061663/06.	
DR	P-PSDB; ADG85245.	
XX		
PT	Novel mutant Chryso sporium strain comprising nucleic acid sequence	
PT	encoding polypeptide of interest such as proteases and lipases, the	
PT	nucleic acid sequence being operably linked to expression-regulating	
PT	region.	
XX		
PS	Disclosure; SEQ ID NO 1; 70pp; English.	
XX		
CC	The invention relates to a mutant Chryso sporium strain comprising a	
CC	nucleic acid sequence encoding a polypeptide of interest. A mutant	
CC	Chryso sporium strain is useful for producing a polypeptide of interest by	
CC	culturing a mutant Chryso sporium strain under conditions permitting	
CC	expression of the protein or polypeptide, and recovering the subsequently	
CC	produced polypeptide of interest. The conditions further permit secretion	
CC	of the protein or polypeptide of interest. The polypeptides are useful	
CC	for hydrolysing beta-glucosidic bonds. A polypeptide is useful for	
CC	hydrolysing beta-xylosidic bonds. The present sequence represents human	
CC	Chryso sporium associated DNA.	
XX		
SQ	Sequence 1570 BP; 553 A; 267 C; 358 G; 392 T; 0 U; 0 Other;	
	Query Match 97.1%; Score 949.8; DB 12; Length 1570;	
	Best Local Similarity 99.8%; Pred. No. 7.5e-250;	
	Matches 951; Conservative 0; Mismatches 2; Indels 0; Gaps 0;	
QY	1 TCTACAACCCATCATAAAAGAAGACAATGAATGATTTTGAATTTGAACTACTAGGT 60	
DB	531 TCTACAACCCATCATAAAAGAAGACAATGAATGATTTTGAATTTGAACTACTAGGT 590	
QY	61 AAAGGCACCTTTGGGAAAGTTATTTGGTTCAGAGAAGCGAAGTGGAAAATCTATGCT 120	
DB	591 AAAGGCACCTTTGGGAAAGTTATTTGGTTCAGAGAAGCGAAGTGGAAAATCTATGCT 650	
QY	121 ATGACGATTTCTGAAGAAGCAAGTTCATTATTGCAAGGATGAAGTGGCACACACTCTAACT 180	
DB	651 ATGACGATTTCTGAAGAAGCAAGTTCATTATTGCAAGGATGAAGTGGCACACACTCTAACT 710	
QY	181 GAAAGCAGAGTATTAAAGAACACTAGACATCCCTTTTAAACATCCCTTGAATATTTCCTTC 240	
DB	711 GAAAGCAGAGTATTAAAGAACACTAGACATCCCTTTTAAACATCCCTTGAATATTTCCTTC 770	
QY	241 CAGACAAAAGACCGTTTGTGTTTGTGATGGAATATGTTAATGGGGCGAGCTGTTTTC 300	
DB	771 CAGACAAAAGACCGTTTGTGTTTGTGATGGAATATGTTAATGGGGCGAGCTGTTTTC 830	
QY	301 CATTTCTCGAGAGCGGGTGTCTCTGAGGACCGCACACGTTTCTATGTCGAGAAATT 360	
DB	831 CATTTCTCGAGAGCGGGTGTCTCTGAGGACCGCACACGTTTCTATGTCGAGAAATT 890	

QY	361 GTCTCTGCTTGGACTATCTACATTTCCGAAAGATTGTGTACCGTGATCTCAAGTTGGAG 420	
DB	891 GTCTCTGCTTGGACTATCTACATTTCCGAAAGATTGTGTACCGTGATCTCAAGTTGGAG 950	
QY	421 AATCTAATGCTGGACAAAGATGGCCACATATAAATTTACAGATTTTGGACTTTGCAAAAGAA 480	
DB	951 AATCTAATGCTGGACAAAGATGGCCACATATAAATTTACAGATTTTGGACTTTGCAAAAGAA 1010	
QY	481 GGGATCACAGATGCAGCCACCACATGAAGACATTTCTGTGGCACTCCAGAAATATCTGGCACCA 540	
DB	1011 GGGATCACAGATGCAGCCACCACATGAAGACATTTCTGTGGCACTCCAGAAATATCTGGCACCA 1070	
QY	541 GAGGTGTTAGAAAGATAATGACTATGCGCCGAGCAGTAGACTGTGGGGCCCTAGGGGTGTGTC 600	
DB	1071 GAGGTGTTAGAAAGATAATGACTATGCGCCGAGCAGTAGACTGTGGGGCCCTAGGGGTGTGTC 1130	
QY	601 ATGTATGAAATGATGCTGTGGGAGGTTTACTCTTTCTACAACCCAGGACCATGAGAAACTTTTTT 660	
DB	1131 ATGTATGAAATGATGCTGTGGGAGGTTTACTCTTTCTACAACCCAGGACCATGAGAAACTTTTTT 1190	
QY	661 GAATTAATATTAATGAAGACATTAATAATTTCTCGAACACTCTCTTTCAGATGCAAAATCA 720	
DB	1191 GAATTAATATTAATGAAGACATTAATAATTTCTCGAACACTCTCTTTCAGATGCAAAATCA 1250	
QY	721 TTGCTTTGAGGCTCTTGATTAAGGATCAATAATAACCGCTTGGTGGAGGACCAAGATGAT 780	
DB	1251 TTGCTTTGAGGCTCTTGATTAAGGATCAATAATAACCGCTTGGTGGAGGACCAAGATGAT 1310	
QY	781 GCAAAAGAAATTTATGAGACACAGATTTCTTCTCTGAGTAAACTGGCAAGATGTATATGAT 840	
DB	1311 GCAAAAGAAATTTATGAGACACAGATTTCTTCTCTGAGTAAACTGGCAAGATGTATATGAT 1370	
QY	841 AAAAGCTTGTACCTCTCTTTTAAACCTCAAGTAACATCTGAGACAGATAGATATTTT 900	
DB	1371 AAAAGCTTGTACCTCTCTTTTAAACCTCAAGTAACATCTGAGACAGATAGATATTTT 1430	
QY	901 GATGAAGAATTTACAGCTCAGCTATTAATAAACCACCACTGGAATAATATGA 953	
DB	1431 GATGAAGAATTTACAGCTCAGCTATTAATAAACCACCACTGGAATAATATGA 1483	

RESULT 14

ADZ49363	ADZ49363 standard; DNA; 1703 BP.
XX	ADZ49363;
AC	ADZ49363;
XX	
DT	30-JUN-2005 (first entry)
XX	
DE	Insulin signaling pathway related gene, SEQ ID 692.
XX	
KW	Antidiabetic; Gene Therapy; Non-insulin dependent diabetes;
KW	insulin resistance; gene; ds.
OS	Homo sapiens.
XX	
PN	US2005085436-A1.
XX	
PD	21-APR-2005.
XX	
PF	08-JUL-2004; 2004US-00887553.
XX	
PR	08-JUL-2003; 2003US-0485883P.
XX	
PA	(LIHH/) LI H.
PA	(MAJU/) MA J.
XX	
PI	Li H, Ma J;
XX	
DR	WPI; 2005-305194/31.
XX	
PT	Treating, preventing or ameliorating pathological conditions associated

PT with dysregulation of the insulin signaling pathway (ISP) comprises  
PT administering to a subject an amount of a modulator of any of the  
PT proteins regulated by ISP.  
XX Disclosure; SEQ ID NO 692; 70pp; English.  
XX The present invention relates to a method for treating, preventing or  
CC ameliorating pathological conditions associated with dysregulation of the  
CC insulin signaling pathway (ISP). The method comprises administering to a  
CC subject a modulator for ISP-regulated proteins or a pharmaceutical  
CC composition comprising the described modulator. The method is useful for  
CC treating, preventing or ameliorating pathological conditions associated  
CC with dysregulation of the ISP such as Type II diabetes or Type A syndrome  
CC of insulin resistance. The present sequence is a human homolog of a  
CC Drosophila gene regulated by ISP. Note: The sequence data for this patent  
CC did not form part of the printed specification, but was obtained in  
CC electronic format directly from USPTO at  
CC seqdata.uspto.gov/sequence.html?docID=20050085436.  
XX

SQ Sequence 1703 BP; 576 A; 316 C; 387 G; 424 T; 0 U; 0 Other;

Query Match 97.1%; Score 949.8; DB 14; Length 1703;  
Best Local Similarity 99.8%; Pred. No. 7.7e-250;  
Matches 951; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TCTACAAACCCATCAATAAAGAAAGACAAATGAATGATTTTGACTATTGAAACTACTAGGT 60  
Db TCTACAAACCCATCAATAAAGAAAGACAAATGAATGATTTTGACTATTGAAACTACTAGGT 546  
Qy 61 AAAGGCACTTTTGGGAAGTTATTTTGGTTCGAGAGAAGGCAAGTGGAAATACTATGCT 120  
Db AAAGGCACTTTTGGGAAGTTATTTTGGTTCGAGAGAAGGCAAGTGGAAATACTATGCT 606  
Qy 121 ATGAAGATCTTGAGAAAGAAGTCAATATTTCGAAAGATGAAGTGGCACACACTCTAACT 180  
Db ATGAAGATCTTGAGAAAGAAGTCAATATTTCGAAAGATGAAGTGGCACACACTCTAACT 666  
Qy 181 GAAAGCAGAGATTATTAAGAACACACTAGACATCCCTTTTAAACATCCTTGAATAATTCCTTC 240  
Db GAAAGCAGAGATTATTAAGAACACACTAGACATCCCTTTTAAACATCCTTGAATAATTCCTTC 726  
Qy 241 CAGACAAAGACCGTTTGTGTGTTTGTGATGGAATATGTTAATGGGCGGAGCTGTTTTTC 300  
Db CAGACAAAGACCGTTTGTGTGTTTGTGATGGAATATGTTAATGGGCGGAGCTGTTTTTC 786  
Qy 301 CATTTGCGAGAGACGGGTGTTCTCTGAGAGACCGCACACGCTTTCTATGGTGCAGAAATT 360  
Db CATTTGCGAGAGACGGGTGTTCTCTGAGAGACCGCACACGCTTTCTATGGTGCAGAAATT 846  
Qy 361 GTCTCTGCTTGGACTATCTACATTCCGGAAGATTGTGTACCGTGATCTCAAGTTGGAG 420  
Db GTCTCTGCTTGGACTATCTACATTCCGGAAGATTGTGTACCGTGATCTCAAGTTGGAG 906  
Qy 421 AATCTAATGCTGGACAAAGATGGCCACATAAAATAACAGATTTTGGACTTTGCAAGAA 480  
Db AATCTAATGCTGGACAAAGATGGCCACATAAAATAACAGATTTTGGACTTTGCAAGAA 966  
Qy 481 GGGATCAGATGAGCCACCATGAGACATCTGTGCGACTCCAGAAATATCTGGACCA 540  
Db GGGATCAGATGAGCCACCATGAGACATCTGTGCGACTCCAGAAATATCTGGACCA 1026  
Qy 541 GAGGTGTTAGAAAGATATGACTATGCGCGACAGTGTAGTGGCGCTAGGGGTTGTC 600  
Db GAGGTGTTAGAAAGATATGACTATGCGCGACAGTGTAGTGGCGCTAGGGGTTGTC 1086  
Qy 601 ATGTATGAAATGATGTGGAGGTTTACCTTTCTACACACGAGCACCATGAGAAATCTTTT 660  
Db ATGTATGAAATGATGTGGAGGTTTACCTTTCTACACACGAGCACCATGAGAAATCTTTT 1146  
Qy 661 GAAATTAATTAATGGAAGACATTAATTTCTCTGAAACACTCTCTCAGATGCAAAATCA 720  
Db GAAATTAATTAATGGAAGACATTAATTTCTCTGAAACACTCTCTCAGATGCAAAATCA 1206

Qy 721 TTGCTTTTCAGGCTCTTTGATAAAGAGATCCAAATAAAGCCTTGTGTGAGACACAGATGAT 780  
Db TTGCTTTTCAGGCTCTTTGATAAAGAGATCCAAATAAAGCCTTGTGTGAGACACAGATGAT 1266  
Qy 781 GCAAAAGAAATATGAGACACAGTTTCTTCTCTGGAGTAAACTGGCAAGATGTATATGAT 840  
Db GCAAAAGAAATATGAGACACAGTTTCTTCTCTGGAGTAAACTGGCAAGATGTATATGAT 1326  
Qy 841 AAAAAGCTTCTACCTCTCTTTTAAACCTCAAGTAACTCTGAGACAGATCTAGATATTTT 900  
Db AAAAAGCTTCTACCTCTCTTTTAAACCTCAAGTAACTCTGAGACAGATCTAGATATTTT 1386  
Qy 901 GATGAAGAAATTTACAGCTCAGACTATTACAAATAACACCACTGAAAAATATGA 953  
Db GATGAAGAAATTTACAGCTCAGACTATTACAAATAACACCACTGAAAAATATGCA 1439  
RESULT 15  
ADN71941  
ID ADN71941 standard; cDNA; 2277 BP.  
XX  
AC ADN71941;  
XX  
DT 12-AUG-2004 (first entry)  
XX  
DE Chicken serine/threonine protein kinase (akt1) encoding cDNA SEQ ID:27.  
XX  
KW kinase pathway inhibitor; anti-prostate cancer;  
KW mitogen-activated protein kinase pathway inhibitor;  
KW MAP kinase pathway inhibitor; prostate cancer inhibitor;  
KW phosphatidylinositol 3-kinase/Akt kinase pathway;  
KW PI3K/Akt kinase pathway; cytosolic; MAP kinase inhibitor;  
KW phosphatidylinositol 3-kinase/Akt kinase inhibitor;  
KW PI3K/Akt kinase inhibitor; androgen receptor inhibitor; prostate cancer;  
KW chicken; serine/threonine protein kinase; akt1; gene; ss.  
XX  
OS Gallus gallus.  
XX  
PH Key Location/Qualifiers  
FT CDS 466..1908  
FT /\*cag= a  
FT /product= "serine/threonine protein kinase (akt1)"  
XX  
PN WO2004041185-A2.  
XX  
PD 21-MAY-2004.  
XX  
PF 31-OCT-2003; 2003WO-US034636.  
XX  
PR 31-OCT-2002; 2002US-0423340P.  
XX  
PA (UYRP ) UNIV ROCHESTER.  
XX  
PI Chang C, Lee Y, Lin W;  
XX  
XX WPI; 2004-390508/36.  
DR P-PSDB; ADN71942.  
XX  
XX Composition useful in the treatment of e.g. prostate cancer comprises a  
FT kinase pathway inhibitor and an anti-prostate cancer compound.  
XX  
PS Disclosure; SEQ ID NO 27; 118pp; English.  
XX  
CC The present invention describes a composition (C1) which comprises a  
CC kinase pathway inhibitor (a) and an anti-prostate cancer compound (b).  
CC Also described: (1) identification of a mitogen-activated protein (MAP)  
CC kinase pathway inhibitor involving incubating an antiandrogen or a  
CC library of molecules with a cell containing an activable MAP kinase  
CC pathway and selecting the molecules which inhibit the activation of the  
CC MAP kinase pathway; and (2) identification of a prostate cancer inhibitor  
CC involving incubating a cell with hydroxyflutamide and potential  
CC inhibitor, and assaying the level of activation of MAP kinase pathway or  
CC phosphatidylinositol 3-kinase (PI3K)/Akt kinase pathway. C1 has



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OM nucleic - nucleic search, using sw model

Run on: February 15, 2006, 05:12:42 ; Search time 3879 Seconds  
(without alignments)  
11796.279 Million cell updates/sec

Title: US-10-601-311-2  
Perfect score: 978  
Sequence: 1 tctacaaccatcataaaag.....atggtatgactgatgcac 978

326  
978  
3

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : EST:  
1: gb\_est1:  
2: gb\_est2:  
3: gb\_est3:  
4: gb\_hc:  
5: gb\_est4:  
6: gb\_est5:  
7: gb\_est6:  
8: gb\_est7:  
9: gb\_gss1:  
10: gb\_gss2:  
11: gb\_gss3:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query			DB	ID	Description
	Score	Match	Length			
C	1	949.8	97.1	1584	4	HSM801048
	2	890	91.0	1440	10	AV399351
	3	818	83.6	1394	10	AV399353
	4	783	80.1	967	5	BUS20318
	5	705.8	72.2	785	6	CA430499
	6	696.8	71.2	766	5	BU703364
	7	685.8	70.1	777	7	CV557292
	8	670	68.5	703	3	BI917703
	9	646.4	66.1	656	6	CAB67933
	10	635	64.9	641	6	CD675747
C	11	613.2	62.7	673	7	CN459710
	12	603.6	61.7	691	6	CF741213
	13	598.8	61.2	675	5	BU055259
	14	594	60.7	594	5	BU790047
	15	593.8	60.7	710	7	CN526605
C	16	590	60.3	590	7	CR854381
	17	586	59.9	586	6	C9433661
	18	572.6	58.5	783	6	CF723245
	19	566.6	57.9	667	6	CF532847
	20	565.2	57.8	630	6	CB247756
C	21	557.6	57.0	820	6	CB320675
	22	552.4	56.5	669	7	CK640105
	23	552.4	56.5	669	7	CK640105
	24	552.4	56.5	669	7	CK640105

23	547.4	56.0	1440	10	AY399352	AY399352 Pan trogl
24	546.6	55.9	579	3	BP36352	BP36352 BP36352
c	25	536.8	54.9	6	CB044388	CB044388 NISC GC04
26	532	54.4	710	5	BU348855	BU348855 604169023
27	528.6	54.0	849	1	AM027388	AM027388 AM027388
28	527	53.9	3724	4	AK028871	AK028871 Mus muscu
29	524	53.6	602	6	CB044389	CB044389 NISC GC04
30	522.8	53.5	675	7	CNS26012	CNS26012 UI-M-HB0-
31	518.2	53.0	651	6	CD351542	CD351542 UI-M-HB0-
32	515	52.7	515	5	BX281089	BX281089 BX281089
33	514.8	52.6	1659	11	DQ046227	DQ046227 Homo sapi
34	514.2	52.6	719	6	CA378893	CA378893 657877 NC
35	511.4	52.3	1654	11	DQ046228	DQ046228 Pan trogl
36	506.2	51.8	798	7	CNS27185	CNS27185 UI-M-HB0-
37	505	51.6	1829	4	BC068106	BC068106 Danio rer
38	504.2	51.6	1848	4	AK040758	AK040758 Mus muscu
39	503.8	51.5	760	7	CK639280	CK639280 UI-M-HO0-
40	492.4	50.3	557	6	CD675547	CD675547 fs25a03.Y
41	488	49.9	1015	1	AL548951	AL548951 AL548951
42	480.8	49.2	3847	4	AK052953	AK052953 Mus muscu
43	479.2	49.0	664	2	BB662483	BB662483 BB662483
44	476	48.7	479	6	CA773193	CA773193 im60H03.Y
45	474.4	48.5	690	7	CN461080	CN461080 UI-M-HB0-

ALIGNMENTS

RESULT 1

HSM801048

LOCUS

HSM801048

1584 bp

mRNA

linear

HTC 16-APR-2005

DEFINITION

Homo sapiens mRNA; cDNA DKFZp434N0250 (from clone DKFZp434N0250).

ACCESSION

AL117525

VERSION

AL117525.1

GI:5912042

KEYWORDS

HTC.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

REFERENCE

1 (bases 1 to 1584)

AUTHORS

Poustka,A., Albert,R., Moosmayer,P., Schupp,I., Wellenreuther,R.,  
Mewes,H.W., Weil,B., Amid,C., Osanger,A., Fobo,G., Han,M. and  
Wiemann,S.

CONSTRM

The German cDNA Consortium

TITLE

Direct Submission

JOURNAL

Submitted (20-JAN-2005) MIPS, Ingolstaedter Landstr.1, D-85764  
Neuherberg, GERMANY

COMMENT

Clone from S. Wiemann, Molecular Genome Analysis, German Cancer  
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;  
sequenced by DKFZ (German Cancer Research Center,  
Heidelberg/Germany) within the cDNA sequencing consortium of the  
German Genome Project. This clone (DKFZp434N0250) is available at  
the RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH in  
Berlin, Germany. Please contact RZPD for ordering:  
http://www.rzpd.de/cgi-bin/products/cl.cgi?CloneID=DKFZp434N0250  
Further information about the clone and the sequencing project is  
available at http://mips.gsf.de/projects/cdna/.

FEATURES

Location/Qualifiers

1..1584

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/organism="Homo sapiens"

/mol\_type="mRNA"

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/db\_xref="taxon:9606"

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/tissue\_type="testis"

/clone\_lib="434 (synonym: htes3). Vector pSporti; host  
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/dev\_stage="adult"

/note="v-akt murine thymoma viral oncogene homolog 3"

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154..1542

gene

CDS

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ORIGIN

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Best Local Similarity	99.8%	Pred.	No. 4.1e-245				
Matches	951	Conservative	0	Mismatches	2	Indels	0
						Gaps	0

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Db 559 TCTACACCCATCATAAAGAAAGACAAATGAATGATTTTGACTATTTGAAACTACTAGGT 618

Qy 61 AAAGCAGCTTTTGGAAAGTTATTTTGGTTCGAGAGAGGCAAGTGGAAATACTATGCT 120

Db 619 AAAGCAGCTTTTGGAAAGTTATTTTGGTTCGAGAGAGGCAAGTGGAAATACTATGCT 678

Qy 121 ATGAAGATTTCTGAAGAAGAAGTCATTATTGTCAAAGGATGAAGTGGCACACACTCTAACT 180

Db 679 ATGAAGATTTCTGAAGAAGAAGTCATTATTGTCAAAGGATGAAGTGGCACACACTCTAACT 738

Qy 181 GAAAGCAGAGTATTAAAGAACACTAGACATCCCTTTTAAATCCTTTGAAATATCTCTTC 240

Db 739 GAAAGCAGAGTATTAAAGAACACTAGACATCCCTTTTAAATCCTTTGAAATATCTCTTC 798

Qy 241 CAGACAAAGACCGTTTGTGTTTGTGATGAATATGTTAATGGGGCGAGCTGTTTTTC 300

Db 799 CAGACAAAGACCGTTTGTGTTTGTGATGAATATGTTAATGGGGCGAGCTGTTTTTC 858

Qy 301 CATTGTGTCAGAGACGGGTGTTCTCTGAGGACCGCACACAGTTTCTATGGTGCAGAAATT 360

Db 859 CATTGTGTCAGAGACGGGTGTTCTCTGAGGACCGCACACAGTTTCTATGGTGCAGAAATT 918

Qy 361 GTCTCTGCTTGGACTATCTACATTCGGAAAGATTGTGACCGTGATCTCAAGTTGGAG 420

Db 919 GTCTCTGCTTGGACTATCTACATTCGGAAAGATTGTGACCGTGATCTCAAGTTGGAG 978

Qy 421 AATCTAATGCTGGCAAGATGGCCACATAAAATTACAGATTTTGGACTTTGCAAAAGAA 480

Db 979 AATCTAATGCTGGCAAGATGGCCACATAAAATTACAGATTTTGGACTTTGCAAAAGAA 1038

Qy 481 GGGATCAGATGCGAGCCACCATGAAGACATTTCTGTGGCACTCCAGAAATATCTGGSCACCA 540

Db 1039 GGGATCAGATGCGAGCCACCATGAAGACATTTCTGTGGCACTCCAGAAATATCTGGSCACCA 1098

Qy 541 GAGGTGTTAGAAGATAATGACTATGCGGACGAGTAGACTGGTGGGGCTAGGGGTTGTC 600

Db 1099 GAGGTGTTAGAAGATAATGACTATGCGGACGAGTAGACTGGTGGGGCTAGGGGTTGTC 1158

Qy 601 ATGTATGAAATGATGTGGGAGGTTACCTTTCTACACACGAGGACCATGAGAACTTTTT 660

Db 1159 ATGTATGAAATGATGTGGGAGGTTACCTTTCTACACACGAGGACCATGAGAACTTTTT 1218

Qy 661 GAAATTAATTAATGGAAGACATTTAAATTTCTCGAACACTCTCTTCAGATGCAAAATCA 720

Db 1219 GAAATTAATTAATGGAAGACATTTAAATTTCTCGAACACTCTCTTCAGATGCAAAATCA 1278

Qy 721 TTGCTTTTCAGGCTCTTGATTAAGATTCCAAATTAAGCCCTTGGTGGAGGACGAGATGAT 780

Db 1279 TTGCTTTTCAGGCTCTTGATTAAGATTCCAAATTAAGCCCTTGGTGGAGGACGAGATGAT 1338

781 GCAAAAGAAATTATGAGACACAGTTTCTCTGGAGTAAACTGGCAAGATGTATATGAT 840

Db 1339 GCAAAAGAAATTATGAGACACAGTTTCTCTGGAGTAAACTGGCAAGATGTATATGAT 1398

Qy 841 AAAAAGCTTGACTCTCTCTTTTAAACCTCAAGTAACTCTGAGACAGATAGATATTTT 900

Db 1399 AAAAAGCTTGACTCTCTCTTTTAAACCTCAAGTAACTCTGAGACAGATAGATATTTT 1458

Qy 901 GATGAAGATTTACAGCTCAGACTATACATTAACACCACTGAAAATATGA 953

Db 1459 GATGAAGATTTACAGCTCAGACTATACATTAACACCACTGAAAATATGCA 1511

RESULT 2

AY399351 1440 bp DNA linear GSS 15-DEC-2003

LOCUS Homo sapiens AKT3 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.

ACCESSION AY399351

VERSION AY399351.1 GI:39755340

KEYWORDS GSS.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 1440)

AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.

TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios

JOURNAL Science 302 (5652), 1960-1963 (2003)

PUBMED 14671302

REFERENCE 2 (bases 1 to 1440)

AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.

TITLE Direct Submission

JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA

COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.

FEATURES

source

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/mol\_type="genomic DNA"

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<1..>1440

/gene="AKT3"

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ORIGIN

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Matches 890; Conservative 0; Mismatches 88; Indels 0; Gaps 0;

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Db 406 TCTACACCCATCATAAAGAAAGACAAATGAATGATTTTGACTATTTGAAACTACTAGGT 465

Qy 61 AAAGGCATTTTGGGAAAGTTATTTTGGTTCGAGAGAGGCAAGTGGAAATACTATGCT 120

Db 466 AAAGGCATTTTGGGAAAGTTATTTTGGTTCGAGAGAGGCAAGTGGAAATACTATGCT 525

Qy 121 ATGAAGATTTCTGAAGAAAGAGTCATTATTGCAAAAGGATGAAGTGGCACACACTCTAACT 180

Db 526 ATGAAGATTTCTGAAGAAAGAGTCATTATTGCAAAAGGATGAAGTGGCACACACTCTAACT 585

Qy 181 GAAAGCAGAGTATTAAAGAAACACTAGACATCCCTTTTAAATCCTTTGAAATATATTCCTTC 240

Db	586	GAAGCAGAGTATTAAGACACATAGACATCCCTTTTAAATCTCTGAAATATCTCTTC	645
Qy	241	CAGACAAAGACCGTTTGTGTGTGATGAATATGTTAATGGGGCGAGCTGTTTTTC	300
Db	646	CAGACAAAGACCGTTTGTGTGTGATGAATATGTTAATGGGGCGAGCTGTTTTTC	705
Qy	301	CATTGTGTGAGAGACGGGTGTTCTCTGAGGACCGCACACAGTCTTATGGTGCAGAAATT	360
Db	706	CATTGTGTGAGAGACGGGTGTTCTCTGAGGACCGCACACAGTCTTATGGTGCAGAAATT	765
Qy	361	GTCTCTGCTTGGACTATCTACATTCGCGAAAGATTGTGTACCGTGATCTCAAGTTGGAG	420
Db	766	GTCTCTGCTTGGACTATCTACATTCGCGAAAGATTGTGTACCGTGATCTCAAGTTGGAG	825
Qy	421	AATCTAATGCTGGACAAAGATGGCCACATAAAATTTACAGATTTTGGACTTTGCAAGAA	480
Db	826	AATCTAATGCTGGACAAAGATGGCCACATAAAATTTACAGATTTTGGACTTTGCAAGAA	885
Qy	481	GGGATCACAGATGCAGCCACACATGAAGACATCTCTGTGGCACTCCAGATATCTGGCACA	540
Db	886	GGGATCACAGATGCAGCCACACATGAAGACATCTCTGTGGCACTCCAGATATCTGGCACA	945
Qy	541	GAGGTGTTAGAGATAATGACTATGCGCGAGCAGTAGACTGTGTGGGCTAGGGGTTGTC	600
Db	946	GAGGTGTTAGAGATAATGACTATGCGCGAGCAGTAGACTGTGTGGGCTAGGGGTTGTC	1005
Qy	601	ATGTATGAAATGATGTGTGGGAGGTTTACCTTTCTACAAACAGGACCATCAGAAAATTTTT	660
Db	1006	ATGTATGAAATGATGTGTGGGAGGTTTACCTTTCTACAAACAGGACCATCAGAAAATTTTT	1065
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Qy	721	TTGCTTTTCAAGGCTCTGATAAGGATCCAAATAAACCGCTTGGTGGAGGACCATGAT	780
Db	1126	TTGCTTTTCAAGGCTCTGATAAGGATCCAAATAAACCGCTTGGTGGAGGACCATGAT	1185
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Qy	841	AAAAAGCTGTACTCTTTTAAACCTCAAGTAAACATCTGAGACAGATCTAGATATTTT	900
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LOCUS	AY399353	1394 bp	DNA linear GSS 15-DEC-2003
DEFINITION	Mus musculus AKT3 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.		
ACCESSION	AY399353		
VERSION	AY399353.1	GI:39755342	
KEYWORDS	GSS.		
SOURCE	Mus musculus (house mouse)		
ORGANISM	Mus musculus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
AUTHORS	1 (bases 1 to 1394) Clark, A.G., Ghanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.J., Adams, M.D. and Cargill, M.		

TITLE	Adams,M.D. and Cargill,M. Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios									
JOURNAL	Science 302 (5652), 1960-1963 (2003)									
PUBMED	14671302									
REFERENCE	2 (bases 1 to 1394)									
AUTHORS	Clark,A.G., Ghanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J., Adams,M.D. and Cargill,M.									
TITLE	Direct Submission									
JOURNAL	Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA									
COMMENT	This sequence was made by sequencing genomic exons and ordering them based on alignment.									
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Best Local Similarity	86.4%; Pred. No. 1.6e-209;									
Matches	845; Conservative 0; Mismatches 133; Indels 0; Gaps 0;									
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Qy	61	AAAGGCACCTTTTGGGAAAGTTATTTTGGTTCGAGAGAGGCAAGTGGAATACTATGCT	120							
Db	420	AAAGGCACCTTTTGGGAAAGTTATTTTGGTTCGAGAGAGGCAAGTGGAATACTATGCT	479							
Qy	121	ATGAAGATCTTGAAGAAAGAGTCATTTATGCAAAAGGATGAAGTGGCACACACTTA	180							
Db	480	ATGAAGATCTTGAAGAAAGAGTCATTTATGCAAAAGGATGAAGTGGCACACACTT	539							
Qy	181	GAAAGCAGAGTATTAAGAAACACATAGACATCCCTTTTAAACATCTTGAATA	240							
Db	540	GAAAGCAGAGTACTAAGAAACACACAGATCAATTTTAAACATCTTGAATA	599							
Qy	241	CAGACAAAGACCGTTTGTGTTTGTGATGGAATATGTTAATGGGGCGAGCTGTTTTTC	300							
Db	600	CAGACAAAGACCGTTTGTGTTTGTGATGGAATATGTTAATGGGGCGAGCTGTTTTTC	659							
Qy	301	CATTGTGCGAGAGCGGGTGTCTCTGAGGACCGCACACAGTTTCTATGTCGACAAAT	360							
Db	660	CATTGTGCGAGAGCGGGTGTCTCTGAGGACCGCACACAGTTTCTATGTCGACAAAT	719							
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Qy	481	GGGATCACAGATGCAGCCACCATGAGACATTTCTGTGGCACTCCAGATATCTGGCACCA	540							
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Qy	541	GAGGTGTTAGAAAGATAATGACTATGCGCGAGCAGTAGACTGTGTGGGCTAGGGGTTGT	600							
Db	900	GAGGTATTAGAAAGATAATGACTATGCGCGAGCCGTGGACTGTGTGGGCTTAGGTGTGT	959							
Qy	601	ATGTATGAAATGATGTGTGGAGGTTTACCTTTTACAAACAGGACCATCAGAAAATCTTTT	660							
Db	960	ATGTATGAAATGATGTGTGAAGGTTTGCCTTTTTCACAAACAGGATCATGAGAAATCTTTT	1019							

Qy	661	GAATTAATATTAATGGAAGACATTAATAATTCCTCGAACATCTCTTCTCAGATGCAAAATCA	720
Db	1020	GAATTAATATTAATGGAAGACATTAATAATTCCTCGAACATCTCTTCTCAGATGCAAAATCA	1079
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Db	1140	NN	1199
Qy	841	AAAAAGCTTGACTCTCTTTTAAACCTCAAGTAACATCTGAGACAGATACCTAGATATTTT	900
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Db	1260	GATGAAGAAATTTACAGCTCAGACTATTACATATACACACCTGAAATATGATGAGAT	1319
Qy	961	GGTATGGACTGCATGGAC	978
Db	1320	GGCATGGACGGCATGGAC	1337
RESULT 4			
BU520318			
LOCUS	BU520318	967 bp	mRNA linear EST 12-SEP-2002
DEFINITION	AGENCOURT_10157385 NIH_MGC_134 Mus musculus cDNA clone		
ACCESSION	BU520318		
VERSION	EST.		
KEYWORDS	EST.		
SOURCE	Mus musculus (house mouse)		
ORGANISM	Mus musculus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.		
AUTHORS	1 (bases 1 to 967)		
TITLE	NIH-MGC http://mgs.nci.nih.gov/.		
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)		
COMMENT	Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgapbs-remail.nih.gov Tissue Procurement: Dr. David Rowe CDNA Library Preparation: Invitrogen Corp CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: L14M14099 Row: 1 Column: 05 High quality sequence start: 16 High quality sequence stop: 729.		
FEATURES			
source	1..967 /organism="Mus musculus" /mol_type="mRNA" /db_xref="taxon:10090" /clone="IMAGE:6518260" /tissue_type="undifferentiated limb" /lab_host="DH10B (phage-resistant)" /clone_lib="NIH_MGC_134" /notes="Vector: pCMV-SPORT6.1; Site1: EcoRV; Site2: NotI; Cloned unidirectionally. Primer: Oligo dr. Average insert size 1.7 kb. Constructed by ResGen, Invitrogen Corp. Note: this is a NIH_MGC Library."		
ORIGIN			
Query Match	80.1%;	Score 783;	DB 5; Length 967;
Best Local Similarity	93.4%;	Pred. No. 4.2e-200;	
Matches 883; Conservative	0; Mismatches 55; Indels 7; Gaps 6;		

Qy	37	TTTGACTATTGTAAGCTACTAGGTAAAGGCACCTTTTGGGAAAGTATTTTGGTTTCGAGAG	96
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Qy	97	AAGCAAGTGGAAATATCTATGCTATCAAGATTTCTGAAGAAGATCATTTATTTGCAAG	156
Db	84	AAGCAAGTGGAAATATCTATGCTATCAAGATTTCTGAAGAAGATCATTTATTTGCAAG	143
Qy	157	GATGAAGTGGCACACACTCTAACTGAAAGCAGAGTATTTAAAGAACACCTAGACATCCCTTT	216
Db	144	GATGAAGTGGCACACACTCTTACTGAAAGCAGAGTACTAAAGAACACACGACATCCATTT	203
Qy	217	TTAACTATCTTTGAAATATTCCTTCAGACAAAAGACCGTTTGTGTGTTTGTGATGGAATAT	276
Db	204	TTAACTATCTTTGAAATATTCCTTCAGACAAAAGACCGTTTGTGTGTTTGTGATGGAATAT	263
Qy	277	GTTAAATGGGGCGGAGCTGTTTTCCTTTCTCGAGAGAGCGGGTGTCTCTGAGGACCGC	336
Db	264	GTTAAATGGGGCGGAGCTGTTTTCCTTTCTCGAGAGAGCGGGTGTCTCTGAGGACCGC	323
Qy	337	ACACGTTTCTATGCTGTCAGAAATTTGCTCTGCTTGGACTATCTACATTCGGGAAAGATT	396
Db	324	ACACGTTTCTATGCTGTCAGAAATTTGCTCTGCTTGGACTATCTACATTCGGGAAAGATT	383
Qy	397	GTGTACCGTGATCTCAAGTTGGAGAAATCTTAATGCTGGACAAAGATGCCACATATAAAATT	456
Db	384	GTGTACCGTGATCTCAAGTTGGAGAAATTTGCTCTGCTTGGACTATCTACATTCGGGAAAGATT	443
Qy	457	ACAGATTTTGGACTTTGCAAGAAGGGATCACAGATGACAGCCACCATGAGACATCTCTGT	516
Db	444	ACGGAATTTTGGGCTTTTGCAGAAAGGGATCACAGATGACAGCCACCATGAGACATCTCTGT	503
Qy	517	GGCACTCCAGAAATATCTGGCACAGAGTCTTAGAAGATAATGACTATGCCGAGCAGTA	576
Db	504	GGCACACAGAGTACCTGGCACAGAGTATTAGAGATAATGACTATGCCGAGCAGT	563
Qy	577	GACTGGTGGGGCTTAGGGTGTTCATGTATGAAATGATGTGGGAGGTTTACCTTTCTAC	636
Db	564	GACTGGTGGGGCTTAGGGTGTTCATGTATGAAATGATGTGGGAGGTTTACCTTTCTAC	623
Qy	637	AACGAGGACCATGAGAAATCTTTTGAATTAATTAATGGAAGACATTAATTTCTCTCGA	696
Db	624	AACGAGGACCATGAGAAATCTTTTGAATTAATTAATGGAAGACATTAATTTCTCTCGA	683
Qy	697	ACACTCTCTTCAGATGCAAAATCATTTCTTACGGGCTCTTGATAAAGGATCCAAATATA	756
Db	684	ACACTCTCTTCAGATGCAAAATCATTTCTTACGGGCTCTTGATAAAGGATCCAA--TAA	741
Qy	757	CGCCTTGGTGAGGACACAGATGATGCAAAAGAAATATGAGACACAG-TTTTCTTCTCTGG	815
Db	742	CGCCTTGGTGAGGACACAGATGATGCAAAAGAAATATGAGGACATAGTTTCTTCTCTGG	801
Qy	816	AGTAAACTGGCAAGATGTATATGATAAAGCTTGTACCTCTTTTAACTCAAGTAAC	875
Db	802	AGTAAACTGGCAAGATGTATATGATAAAGCTTGTACCTCTTTTAACTCAAGTAAC	861
Qy	876	ATCTGAGACAGATA-CTAGATATTTTGTAGTAAG-AAATTACAGCTCAGACTATTACATA	933
Db	862	ATCTGAAACAGACACCCCGATATTTTGTAGTAAGAAATTTACAGCTCAGACTATTACATA	921
Qy	934	ACACCACTGAAATATATGATGAGGATGGTATGGACTGGCATGGAC	978
Db	922	ACACCACTGAAATATGATGAGGATGGATGGATGGATGGATGGATGGATGGATGGATGGAC	966
RESULT 5			
CA430499/c			
LOCUS	CA430499	785 bp	mRNA linear EST 07-NOV-2002
DEFINITION	UT-H-FH1-bft-c-24-0-UI.s1 NCI CGAP_FH1 Homo sapiens cDNA clone		
ACCESSION	CA430499		
VERSION	CA430499.1		
KEYWORDS	EST.		

SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homiidae; Homo.  
 1 (bases 1 to 785)  
 NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 Unpublished (1997)  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-r@mail.nih.gov  
 Tissue procurement: James Martin  
 CDNA Library preparation: Dr. M. Bento Soares, University of Iowa  
 CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
 Clone Distribution: Clone distribution information can be obtained  
 from Dr. M. Bento Soares, bento-soares@iowa.edu  
 The following repetitive elements were found in this cDNA  
 sequence: 1-42, sAT rich#Low complexity (matched complement)  
 Seq primer: M13 FORWARD  
 POLYA=Yes.

Location/Qualifiers  
 1..785  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="UI-H-FH1-bft-c-24-0-UI"  
 /tissue\_type="Cell Line"  
 /dev\_stage="Adult"  
 /lab\_host="DH10B (Life Technologies)"  
 /clone\_lib="NCI-CGAP\_FH1"  
 /note="Organ: Chondrosarcoma; Vector: pTT73-Pac  
 (Pharmacia) with a modified polylinker; Site 1: Ecor I;  
 Site 2: Not I; NCI CGAP FH1 is a normalized cDNA library  
 obtained from a cell line derived from grade I  
 chondrosarcoma tissue. The library was constructed and  
 normalized according to Bonaldo, Lennon and Soares, Genome  
 Research, 6:791-806, 1996. First strand cDNA synthesis was  
 primed with an oligo-dT primer containing a Not I site.  
 Double stranded cDNA was ligated to an Ecor I adaptor,  
 digested with Not I, and cloned directionally into  
 pTT73-Pac vector. The oligonucleotide used to prime the  
 synthesis of first-strand cDNA contains a library tag  
 sequence that is located between the Not I site and the  
 (dT)18 tail. The sequence tag for this library is  
 AGAATCCGGC. The cell line was provided by Dr. James Martin  
 from the University of Iowa.  
 TAG\_TISSUE=Human Chondrosarcoma Cell Line CS8 - Grade 1  
 Chondrosarcoma  
 TAG\_LIB=UI-H-FH1  
 TAG\_SEQ=AGAATCCGGC"

ORIGIN  
 Query Match 72.2%; Score 705.8; DB 6; Length 785;  
 Best Local Similarity 99.3%; Pred. No. 2.9e-179;  
 Matches 707; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 242 AGACAAAGACCGTTGTGTTGATGGAATATGTAATGGGGCGAGCTGTTTTC 301  
 DB 785 AGACAAAGACCGTTGTTGATGGAATATGTAATGGGGCGAGCTGTTTTC 726

QY 302 ATTGTGCGAGAGCGGGTGTCTCTGAGGACCGCACACGTTTCTATGTCGAGAAATTG 361  
 DB 725 ATNTGTCGAGAGCGGGTGTCTCTGAGGACCGCACACGTTTCTATGTCGAGAAATTG 666

QY 362 TCTCTGCTTGGACTATCTACATTCGGAAGAGTTGTGTACCGTGATCTCAAGTTGGAGA 421  
 DB 665 TCTCTGCTTGGACTATCTACATTCGGAAGAGTTGTGTACCGTGATCTCAAGTTGGAGA 606

QY 422 ATCTAATGCTGGCAAGATGGCCACATAAAATTAACAGATTTTGACATTTTGAAGAG 481  
 DB 605 ATCTAATGCTGGCAAGATGGCCACATAAAATTAACAGATTTTGACATTTTGAAGAG 546

QY 482 CGATCAGATGCAGCCACCATGAAGACATTTCTGGCACTCCAGAAATATCTGGCACCAG 541  
 DB 545 CGATCAGATGCAGCCACCATGAAGACATTTCTGTGGCACTCCAGAAATATCTGGCACCAG 486

QY 542 AGGTGTTAAGAGATAATGACTATATGCGCGAGCAGTAGACTGTGGGGCCCTAGGGGTTGTCA 601  
 DB 485 AGGTGTTAAGAGATAATGACTATATGCGCGAGCAGTAGACTGTGGGGCCCTAGGGGTTGTCA 426

QY 602 TGTATGAAATGATGTGGGAGGTTACTTCTTCAACACAGGACCATGAGAAATCTTTTGG 661  
 DB 425 TGTATGAAATGATGTGGGAGGTTACTTCTTCAACACAGGACCATGAGAAATCTTTTGG 366

QY 662 AATTAATATTATGAACACATTAATTTCTTCGAACTCTCTTCAGATGCAAAATCAT 721  
 DB 365 AATTAATATTATGAACACATTAATTTCTTCGAACTCTCTTCAGATGCAAAATCAT 306

QY 722 TGCTTTACAGGGCTCTTTGATAAGGATCCAAATFAAACGGCTTGGTGGAGACAGATGATG 781  
 DB 305 TGCTTTACAGGGCTCTTTGATAAGGATCCAAATFAAACGGCTTGGTGGAGACAGATGATG 246

QY 782 CAAAGAAATTAAGACACAGATTTCTCTCTCGAGTAAACTGGCAAGATGATATGATA 841  
 DB 245 CAAAGAAATTAAGACACAGATTTCTCTCTCGAGTAAACTGGCAAGATGATATGATA 186

QY 842 AAAAGCTTGATACCTCTTTTAAACCTCAAGTAAACATCTGAGACAGATAGATATTTTG 901  
 DB 185 AAAAGCTTGATACCTCTTTTAAACCTCAAGTAAACATCTGAGACAGATAGATATTTTG 126

QY 902 ATGAAGAATTTACAGCTCAGACTATTACAATAACACCACTGAAAAATATGA 953  
 DB 125 ATGAAGAATTTACAGCTCAGACTATTACAATAACACCACTGAAAAATATGA 74

RESULT 6  
 BU703964  
 LOCUS 766 bp mRNA linear EST 15-JUL-2003  
 DEFINITION UI-M-F00-bzr-i-04-0-UI.r1 NIH\_BMAP\_F00 Mus musculus cDNA clone  
 IMAGE:6406347 5', mRNA sequence.  
 BU703964  
 ACCESSION BU703964.1 GI:23631576  
 VERSION  
 KEYWORDS  
 SOURCE Mus musculus (house mouse)  
 ORGANISM  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
 Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 766)  
 NIH-MGC <http://mgs.nci.nih.gov/>.  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-r@mail.nih.gov  
 Tissue procurement: Dr. Jim Lin, University of Iowa  
 CDNA Library preparation: Dr. M. Bento Soares, University of Iowa  
 CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
 Clone Distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
 This clone was contributed by the Brain Molecular Anatomy Project  
 (BMAP)  
 Seq primer: pYX-5.  
 Location/Qualifiers  
 1..766  
 /organism="Mus musculus"  
 /mol\_type="mRNA"  
 /strain="C57BL/6"  
 /db\_xref="taxon:10090"  
 /clone="IMAGE:6406347"  
 /tissue\_type="whole brain"  
 /dev\_stage="embryo 12.5dpc"  
 /lab\_host="DH10B (T1 phage resistant)"

FEATURES  
 source

/clone\_lib="NIH\_BMAP\_F00"  
/note="Organ: Brain; Vector: pYX-Asc; Site\_1: EcoR I;  
Site\_2: Not I; The library was constructed according  
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,  
1996. Denatured RNA was size fractionated on a 1% agarose  
gel. First strand cDNA synthesis was primed with oligo-dT  
primer containing a Not I site. Double strand cDNA was  
size selected according to mRNA size fraction, ligated  
with EcoR I adaptor, digested with NotI and then cloned  
directionally into pYX-Asc vector. The library tag  
is TGAGAGACC. This library was created for the University  
Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the  
Developing Mouse Nervous System', supported by National  
Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,  
program coordinator."

ORIGIN

Query Match		71.2%;	Score 696.8;	DB 5;	Length 766;
Best Local Similarity		94.3%;	Pred. No. 7.7e-177;		
Matches 722;		Conservative 0;	Mismatches 44;	Indels 0;	Gaps 0;
Qy	74	GGAAAGTATTTTGGTTCGAGAGAGCGCAAGTGGAAATACTACTGCTATGAGATTCTGA	133		
Db	1	GGAAAGTATTTTGGTTCGAGAGAGCGCAAGTGGAAATACTACTGCTATGAGATTCTGA	60		
Qy	134	AGAAAGAGTCAATTAATGCAAGGATGAAGTGGCACACACTCTAACTGAAAGCAGAGTAT	193		
Db	61	AGAAAGAGTCAATTAATGCAAGGATGAAGTGGCACACACTCTTACTGAAAGCAGAGTAC	120		
Qy	194	TAAAGAACATPAGACATCCCTTTTAAACATCCTTTGAAATATTCCTTCCAGACAAAGACC	253		
Db	121	TAAAGAACACCCAGACATCCATTTTAAACATCCTTTGAAATATTCCTTCCAGACAAAGACC	180		
Qy	254	GTTTGTGTTTTGTCATGGAATATGTTAATGGGGCGAGCTGTTTTCCATTTGTCGAGAG	313		
Db	181	GTTTGTGTTTTGTCATGGAATATGTTAATGGCGGAGAGCTGTTTTCCATTTGTCGAGAG	240		
Qy	314	AGCGGTGTTCTCTGAGGACCGCACACGTTTCTATGTTGTCAGAAATGTCTCTCGCTTGG	373		
Db	241	AGCGAGTGTCTCTGAGGACCGCACACGTTTCTATGTTGTCAGAAATGTCTCTCGCTTGG	300		
Qy	374	ACTATCTACATTCGGAAGAATGTGTACCGTGATCTCAAGTTGGAGAAATCAATGCTGG	433		
Db	301	ACTATCTACATTCGGAAGAATGTGTACCGTGATCTCAAGTTGGAGAAATTTGATGCTAG	360		
Qy	434	ACAAGATGGCCACATATAAATTTACAGATTTTGACATTTTGACATTTGCAAGAAGGATCACAGT	493		
Db	361	ATNAGGATGGCCATATAAATTTACGATTTTGGGCTTTGCAAGAAGGATCACAGAT	420		
Qy	494	CAGCCACCATGAAGACATCTCTGGCACTCCAGAAATATCTGGCACCGAGAGTGTAGAG	553		
Db	421	CAGTACCATGAGACATCTCTGGCACACAGATACCTGGCACCGAGAGTATTAGAG	480		
Qy	554	ATAATGACTATGGCGAGCAGTAGATGGTGGGCGCTAGGGGTTGTCTATGATGAATGA	613		
Db	481	ATAATGACTATGGCGAGCAGTAGATGGTGGGCGCTAGGGGTTGTCTATGATGAATGA	540		
Qy	614	TGTGTGGAGGTTACCTTTCTACACCGAGGACCATGAGAACTTTTGAATTAATATA	673		
Db	541	TGTGTGGAGGTTGCTTTCTACACCGAGGATCATGAGAACTCTTTGAATTAATATA	600		
Qy	674	TGGAAGACATTAATTTCTCGAACACATCTCTTCAGATGCAAAATCATTTGCTTTTCAGGGC	733		
Db	601	TGGAAGACATTAATTTCTCGAACACATCTCTTCAGATGCAAAATCATTTGCTTTTCAGGGC	660		
Qy	734	TCATTGATAAAGGATCCAAATAAAGCCCTTGGTGGAGGACCCAGATGATGCAAAAGAAATTA	793		
Db	661	TCATTGATAAAGGATCCANATAAAGCCCTTGGTGGAGGACCCAGATGATGCAAAAGAAATCA	720		
Qy	794	TGAGACACAGTTTCTCTCTGGAGTAAACTGGCAAGATGTTATATGA	839		
Db	721	TGAGGCATAGTTTTTTTTTCTGGAGTAAACTGGCAAGATGTTATATGA	766		

RESULT 7

CV557292

LOCUS

DEFINITION

CV557292

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Mus musculus

Mus musculus (house mouse)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 777)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. James Lin University of Iowa

cDNA Library preparation: Dr. M. Bento Soares, University of Iowa

cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Distribution information can be found at

http://genome.uiowa.edu/distribution/mousefl.html

This clone was contributed by the Brain Molecular Anatomy Project

(BMAP)

Seq primer: pYX-5.

Location/Qualifiers

1. 777

/organism="Mus musculus"

/mol\_type="mRNA"

/strain="C57BL/6"

/db\_xref="taxon:10090"

/dev\_stage="newborn 1,5,15 and embryos 15,16,17,18 dpc"

/tissue\_type="whole eye"

/lab\_host="DH10B (T1 phage resistant)"

/clone\_lib="NIH\_BMAP\_H20"

/notes="Organ: Eye; Vector: pYX-Asc; Site\_1: EcoR I;

Site\_2: Not I; The library was constructed according

Bonaldo, Lennon and Soares, Genome Research, 6:791-806,

1996. Denatured RNA was size fractionated on a 1% agarose

gel. First strand cDNA synthesis was primed with oligo-dT

primer containing a Not I site. Double strand cDNA was

size selected according to mRNA size fraction, ligated

with EcoR I adaptor, digested with NotI and then cloned

directionally into pYX-Asc vector. The library tag

is AATAATTACG. This library was created for the University

Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the

Developing Mouse Nervous System', supported by National

Institute of Mental Health (NIMH)."

ORIGIN

Query Match

Best Local Similarity

Matches 722;

Conservative 0;

Mismatches 50;

Indels 1;

Gaps 1;

Qy

107

GAAATATCTATGCTATGAAGATTCCTGAAGAAAGAAAGTCATTATTGCAAAAGGATGAAGTGG

166

6

GGAAATCTATGCTATGAAGA-TCTGAAGAAAGAAAGTCATTATTGCAAAAGGATGAAGTGG

64

Qy

167

CACACATCTTAAGTGAAGCAGAGTATTAAGACACTAGACATCCCTTTTACATCCCT

226

Db

65

CACACATCTTACTGAAGCAGAGTACTAAAGAACACACAGACATCCATTTTACATCCT

124

Qy

227

TGAATATTTCTTCCAGACAAAGACCGTTTGTGTTTGTGATGGAATATGTTAATGGG

286

Db

125

TGAATATTTCTTCCAGACAAAGACCGTTTGTGTTTGTGATGGAATATGTTAATGGG

184

287	Qy	GGGAGCTGTTTTTCCATTTTGTGAGAGCGGGTGTCTCTGAGGACCGCACAGTTTCT	346
185	Db	GAGAGCTGTTTTTCCATTTGTGAGAGCGAGTGTCTCTGAGGACCGCACAGTTTCT	244
347	Qy	ATGGTGCAGAAATCTGCTCTGCTTGGACTATCTACATTCGGGAAGATTGTGTACCGTG	406
245	Db	ATGGTGCAGAAATGTGCTCTGCTTTGGACTATCTACATTTGGAAAGATTGTGTACCGTG	304
407	Qy	ATCTCAAGTTGGAGAATCTAATGCTGGGCAAAAGATGCCCATATAAAATTTACAGATTTTG	466
305	Db	ATCTCAAGTTGGAGAATTTGATGCTAGATAAGGATGCCCATATAAAATTTACGATTTTG	364
467	Qy	GACTTTGCAAAAGAGGATCACAGATGCAGGCCACCATGAAGACATCTCTGTGGCACTCCAG	526
365	Db	GGCTTTGCAAAAGAGGATTCAGATGCAGTCCATGAAGACATCTCTGTGGCACACGAG	424
527	Qy	AATATCTGCGCACGAGGTGTTAGAAAGATAATGACTATGCGCGAGCAGTAGACTGTGTGG	586
425	Db	AGTACCTGCGCACGAGGTATTTAGAAGATATGACTATGCGCGAGCCGTGACTGTGTGG	484
587	Qy	GCCTAGGGTGTCTATGTATGAATGTGTGTGGAGGTTACCTTTCTACAACCAGGACC	646
485	Db	GCTTAGGTGTCTATGTATGAATGTGTGTGAAGGTTGCCCTTTCTACAACCCAGGATC	544
647	Qy	ATGAGAACTTTTTCGAAATTAATATGGAAGACATTAATAATTTCTCGAACACTCTCTT	706
545	Db	ATGAGAACTCTTTGAAATTAATCTAATATGGAAGACATTAATAATTTCCCCCGAACACTCTCTT	604
707	Qy	CAGATGCAAAATCATTTGCTTTTCAGGGCTCTTGATAAAGGATCCAAATAAAGCCTTTGGTG	766
605	Db	CAGATGCANNAATCATTTGCTTTTCAGGGCTCTTTGATAAAGGATCCANNAAGCCTTTGGTG	664
767	Qy	GAGGACCGATGATCAAAAGAAATTTATGAGACACAGTTTCTTCTCTGGAGTAAACTGGC	826
665	Db	GAGGACCGATGATGCANAAAGAAATCATAGGACATAGTTNTTTTCTGGAGTANAATGGC	724
827	Qy	AAGATGTATATGATATAAAAGCTTGATCCTCTCTTTTAAACCTCAAGTAAACATCT	879
725	Db	ANGATGTATATGACAAAAGCTTGATCCTCTCTTTTAANGCTCAAGTAAACATCT	777

RESULT 8	703 bp	linear	EST 16-OCT-2001
BI917703	603183679F1 NIH_MGC_121	Homo sapiens cDNA clone IMAGE:5247930 5',	
LOCUS			
DEFINITION			
ACCESSION	BI917703		
VERSION	BI917703.1	GI:16181501	
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;		
	Hominidae; Homo.		
REFERENCE	1 (bases 1 to 703)		
AUTHORS	NIH-MGC <a href="http://mgc.nci.nih.gov/">http://mgc.nci.nih.gov/</a> .		
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)		
JOURNAL	Unpublished (1999)		
COMMENT	Contact: Robert Strausberg, Ph.D. Email: <a href="mailto:cgapbs-r@mail.nih.gov">cgapbs-r@mail.nih.gov</a> Tissue Procurement: Life Technologies, Inc. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <a href="http://image.llnl.gov">http://image.llnl.gov</a> Plate: LLAM11625 row: m column: 19 High quality sequence stop: 703.		

FEATURES  
source

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L. : 703
/organism="Homo sapiens"
/mol type="mRNA"
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CA867933  
LOCUS  
DEFINITION

CA867933  
ir83c04.

656 bp mRNA linear EST 20-DEC-2002  
no sapiens cDNA clone IMAGE:6608840 5'

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/db_xref="taxon:9606"
/clone="IMAGE:5247930"
/lab_host="DH10B"
/clone_lib="NIH_MGC_121"
/note="Organ: brain; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA source anonymous pool of 3 fetal brains, female age 20 weeks, female age 24 weeks, and male age 26 weeks. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.7 kb, insert size range 0.7-3.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 017. Note: this is a NIH MGC Library."

```

## ORIGIN

Query Match	68.5%;	Score 670;	DB 3;	Length 703;
Best Local Similarity	99.7%;	Pred. No. 1.3e-169;		
Matches 692;	Conservative 0;	Mismatches 0;	Indels 2;	Gaps 2;
QY	278	TTAATGGGCGGAGCTGTTTCTTCATTTGTCGAGAGAGCGGGTCTCTCTGAGGACCGCA	337	
DB	1	TTAATGGGCGGAGCTGTTTCTTCATTTGTCGAGAGAGCGGGTCTCTCTGAGGACCGCA	60	
QY	338	CAGCTTCTATGGTCGAGAAATGTCTCTGCTTGGACTATCTACATTCGCGAAAGATTG	397	
DB	61	CAGCTTCTATGGTCGAGAAATGTCTCTGCTTGGACTATCTACATTCGCGAAAGATTG	120	
QY	398	TGTAACGCTGATCTCAAGTTGGAGAACTTAATGCTGGACAAAGATGGCCACATATAAAATTA	457	
DB	121	TGTAACGCTGATCTCAAGTTGGAGAACTTAATGCTGGACAAAGATGGCCACATATAAAATTA	180	
QY	458	CAGATTTTGGACTTTGCCAAGAGGGATCACAGATGCAGCCACCATGAGACATTTCTGTG	517	
DB	181	CAGATTTTGGACTTTGCCAAGAGGGATCACAGATGCAGCCACCATGAGACATTTCTGTG	240	
QY	518	GCACCTCCAGAAATATCTGGCCACGAGGGTTAGAAGATATGACTATGGCGGAGCAGTAG	577	
DB	241	GCACCTCCAGAAATATCTGGCCACGAGGGTTAGAAGATATGACTATGGCGGAGCAGTAG	300	
QY	578	ACTGTGTGGGCGCTAGGGGTTGTCATGTATGAATATGATGTGGAGGTTACCTTTCTACA	637	
DB	301	ACTGTGTGGGCGCTAGGGGTTGTCATGTATGAATATGATGTGGAGGTTACCTTTCTACA	360	
QY	638	ACCAGGACCATGGAACCTTTTGAATTAATTAATGGAAGACATTAATTTCCCTCGAA	697	
DB	361	ACCAGGACCATGGAACCTTTTGAATTAATTAATGGAAGACATTAATTTCCCTCGAA	420	
QY	698	CACCTCTCTCAGATGCAGAAATCATCTGCTTTCAGGGCTCTTGATAAAGGATCCAAATAAAC	757	
DB	421	CACCTCTCTCAGATGCAGAAATCATCTGCTTTCAGGGCTCTTGATAAAGGATCCAAATAAAC	480	
QY	758	GCCTTGGTGGAGGACGAGATGATGCAAAAAGAAATATGAGACACAGTTTCTTCTCGAG	817	
DB	481	GCCTTGGTGGAGGACGAGATGATGCAAAAAGAAATATGAGACACAGTTTCTTCTCGAG	540	
QY	818	TAAACTGGCAAGATGTATGATATAAAGCTTGACCTCCTTTTAAACCTCAAGTACAT	877	
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QY	878	CTGAGACAGATCTAGATATTTTGGTGAAGAAATTTACAGCTCAGACTATTTACAATAACAC	937	
DB	601	CTGAGACAGATCTAGATATTTTGGTGAAGAAATTTACAG-TCAGACTATTTACAATAACAC	659	
QY	938	CACCTGAAAAATATGATAGGATGGTATGACTG	971	
DB	660	CA-CTGAAAAATATGATAGGATGGTATGACTG	692	

## RESULT 9

RESULT 9  
CA867933

similar to TR:Q9Y243 Q9Y243 PROTEIN KINASE B GAMMA. ;, mRNA sequence.

ACCESSION CA867933  
VERSION CA867933.1 GI:27319482

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae; Homo.

REFERENCE 1 (bases 1 to 656)

Melton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K., Lemishka, I., Scarce, M., Brestelli, J., Gradwohl, G., Clifton, S., Hillier, L., Marra, M., Pape, D., Wylie, T., Martin, J., Blissett, A., Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J., Cardenas, M., Gibbons, M., McCann, R., Cole, R., Tsagaris, V., Williams, T., Jackson, Y., and Bowers, Y.

Endocrine Pancreas Consortium

Unpublished (2000)

Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue

Endocrine Pancreas Consortium

Harvard University, Howard Hughes Medical Institute

Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge, MA 02138

Tel: 617-495-1812

Fax: 617-495-8557

Email: dmelton@biohp.harvard.edu

Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:

Washington University Genome Sequencing Center For information on

obtaining a clone please contact: Dr. Hiroshi Inoue

(hinoue@im.wustl.edu)

Seq primer: -40UP from Gibco

High quality sequence stop: 486.

Location/Qualifiers

FEATURES

source

1..656

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clones="IMAGE:6608840"

/tissue\_type="Purified pancreatic islet"

/lab\_host="DH10B"

/clone\_lib="HR85 islet"

/note="Organ: Pancreas; Vector: pBluescript SK(-); Site: 1: NotI; Site 2: XhoI; cDNA made by oligo-dT priming.

Size-selected on agarose gel. Average insert size -1kb. 5'

XhoI site was destroyed after directional cloning.

Amplified once. Contact information: Hiroshi Inoue, MD,

Metabolism Div. (Alan Permutt Lab), Washington University

School of Medicine, Box 8127, 660 South Euclid Ave., St.

Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel:

314-362-1916, Fax: 314-747-2692."

ORIGIN

Query Match 66.1%; Score 646.4; DB 6; Length 656;

Best Local Similarity 99.8%; Pred. No. 3e-163;

Matches 647; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

211 CCCTTTTACATCCTTGAATATTCCTCCAGACAAAGACCGTTGTCTTTGTGATG 270

9 CGCTTTTAAACATCCTTGAATATTCCTCCAGACAAAGACCGTTGTGTGTGATG 68

271 GAATATGTTAATGGGGCGAGCTGTTTTCATTTGTCGAGAGCGGTGTTCTCTGAG 330

69 GAATATGTTAATGGGGCGAGCTGTTTTCATTTGTCGAGAGCGGTGTTCTCTGAG 128

331 GACCGCACACCTTTCTATGTCGAGAAATTTGCTCTGCTGGGACTATCTACATTCGCGA 390

129 GACCGCACACCTTTCTATGTCGAGAAATTTGCTCTGCTGGGACTATCTACATTCGCGA 188

391 AAGATTGTGACCTGATCTCAAGTGGAGATCTAATGCTGGCAAGATGGCCACATA 450

189 AAGATTGTGACCTGATCTCAAGTGGAGATCTAATGCTGGCAAGATGGCCACATA 248

Qy 451 AAAATTACAGATTTTGGACTTTGCAAAAGAGGATCAAGATGAGCCATGAGGATCAAGACA 510

Db 249 AAAATTACAGATTTTGGACTTTGCAAAAGAGGATCAAGATGAGCCATGAGGATCAAGACA 308

Qy 511 TTCTGTGGCACTCCAGAAATATCTGGCACAGAGGTGTTAGAGATAATAGCTATGGCGGA 570

Db 309 TTCTGTGGCACTCCAGAAATATCTGGCACAGAGGTGTTAGAGATAATAGCTATGGCGGA 368

Qy 571 GCAGTAGACTGGTGGGCTAGGGGTTGTCATGATGAAATGATGTGGGAGGTACCT 630

Db 369 GCAGTAGACTGGTGGGCTAGGGGTTGTCATGATGAAATGATGTGGGAGGTACCT 428

Qy 631 TTCTACAACAGGACCATGAAACCTTTTGAATTAATTAATGGAAGACATTAATTT 690

Db 429 TTCTACAACAGGACCATGAAACCTTTTGAATTAATTAATGGAAGACATTAATTT 488

Qy 691 CCTCGAACACTCTCTTCAGATGCAAAATCATTTGCTTTTCAGGGCTCTTGATAAAGATCCA 750

Db 489 CCTCGAACACTCTCTTCAGATGCAAAATCATTTGCTTTTCAGGGCTCTTGATAAAGATCCA 548

Qy 751 AATAAAGCGCTTGGTGGAGGACCATGATGCAAAAGAAATTAATGAGACACAGTTTCTTC 810

Db 549 AATAAAGCGCTTGGTGGAGGACCATGATGCAAAAGAAATTAATGAGACACAGTTTCTTC 608

Qy 811 TCTGGAGTAAACTGGCAAGATGTATATGATAAAGCTTTGACCTCT 858

Db 609 TCTGGAGTAAACTGGCAAGATGTATATGATAAAGCTTTGACCTCT 656

RESULT 10

CD675747

LOCUS

DEFINITION

fs27d11.y1 Human Lens cDNA (Normalized): fs Homo sapiens cDNA clone

fs27d11.5', mRNA sequence.

ACCESSION CD675747

VERSION CD675747.1 GI:32177478

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Homidae; Homo.

REFERENCE 1 (bases 1 to 641)

Wistow, G., Bernstein, S.L., Wyatt, M.K., Behal, A., Touchman, J.W.,

Bouffard, G., Smith, D. and Peterson, K.

Expressed sequence tag analysis of adult human lens for the NEBank

Project: over 2000 non-redundant transcripts, novel genes and

splice variants

Mol. Vis. 8 (4), 171-184 (2002)

12107413

COMMENT

Contact: Wistow G

Section on Molecular Structure and Function

National Eye Institute

6/331, NIH, Bethesda, MD 20892-2740, USA

Tel: 301 402 3452

Fax: 301 496 0078

Email: graeme@helix.nih.gov

Plate: 27 row: d column: 11

Seq primer: M13RP1 reverse primer (ABI).

Location/Qualifiers

1..641

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="fs27d11"

/tissue\_type="Lens"

/dev\_stage="Adult"

/lab\_host="EMDH10B"

/clone\_lib="Human Lens cDNA (Normalized): fs"

/note="Organ: Eye; Vector: pCMVSPORT6; A human lens

library (by) was normalized by self-subtraction. One

portion of double stranded plasmid DNA representing the

library was linearized by NotI. This NotI digested library



was used as a template for biotinylated RNA synthesis using SP6 RNA polymerase. Another portion of the double stranded plasmid library was converted to single-stranded circles in vitro using Gene II and Exonuclease III (Life Technologies). Single-stranded DNA (1 mg) was hybridized (Cot 500) with 41 mg of Bio-RNA and vector blocking oligonucleotides. The hybridized Bio-RNA/ss-circles were removed by streptavidin:phenol extraction. EST analysis was performed on the library at the NIH Intramural Sequencing Center (NISC)."

ORIGIN

Query Match	64.9%;	Score 635;	DB 6;	Length 641;
Best Local Similarity	100.0%;	Pred. No. 3.6e-160;	Indels 0;	Gaps 0;
Matches 635;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	TCTACACCCCATCATATAAAGAAAGCAATGATGATTTTGGACTATTTGAACTACTAGGT	60	
Db	7	TCTACACCCCATCATATAAAGAAAGCAATGATGATTTTGGACTATTTGAACTACTAGGT	66	
Qy	61	AAAGGCACTTTTGGGAAAGTTATTTTGGTTTCGAGAGAGGCGAAGTGGGAAATATCTATGCT	120	
Db	67	AAAGGCACTTTTGGGAAAGTTATTTTGGTTTCGAGAGAGGCGAAGTGGGAAATATCTATGCT	126	
Qy	121	ATGAGATTCTCAAGAAAGAGTCAATATTCGAAGGATGAAGTGGGCACACTCTAACT	180	
Db	127	ATGAGATTCTCAAGAAAGAGTCAATATTCGAAGGATGAAGTGGGCACACTCTAACT	186	
Qy	181	GAAAGCAGATATTAAAGAAACATAGACATCCCTTTTAAATCTCTGAAATATTCCTTC	240	
Db	187	GAAAGCAGATATTAAAGAAACATAGACATCCCTTTTAAATCTCTGAAATATTCCTTC	246	
Qy	241	CAGACAAAGACCGTTTGTGTTTGTGATGAATATGTAATGAGGCGGAGCTGTTTTTC	300	
Db	247	CAGACAAAGACCGTTTGTGTTTGTGATGAATATGTAATGAGGCGGAGCTGTTTTTC	306	
Qy	301	CATTGTGCGAGAGCGGGTGTCTCTGAGGACCGCACACGTTTCTATGTTGCGAATTT	360	
Db	307	CATTGTGCGAGAGCGGGTGTCTCTGAGGACCGCACACGTTTCTATGTTGCGAATTT	366	
Qy	361	GTCTCTGCTTGGACTATCTACATTCGGAAGATTGTGTACCGTGATCTCAAGTTGGAG	420	
Db	367	GTCTCTGCTTGGACTATCTACATTCGGAAGATTGTGTACCGTGATCTCAAGTTGGAG	426	
Qy	421	AATCTAATGCTGGACAAAGATGGCCACATAAAATTCAGATTTTGGACTTTGCAAGAA	480	
Db	427	AATCTAATGCTGGACAAAGATGGCCACATAAAATTCAGATTTTGGACTTTGCAAGAA	486	
Qy	481	GGGATCAGATGCGAGCACCACATGAAGACATCTGTGGCCTCCAGATATCTGGCACC	540	
Db	487	GGGATCAGATGCGAGCACCACATGAAGACATCTGTGGCCTCCAGATATCTGGCACC	546	
Qy	541	GAGGTGTTAGAGATAATGACTATGCGCGAGCAGTAGACTGTGGGGCTTAGGGGTTGTC	600	
Db	547	GAGGTGTTAGAGATAATGACTATGCGCGAGCAGTAGACTGTGGGGCTTAGGGGTTGTC	606	
Qy	601	ATGATGAAATGATGTGGGAGGTTTACCTTTCTA	635	
Db	607	ATGATGAAATGATGTGGGAGGTTTACCTTTCTA	641	

RESULT 11

CN459710	
LOCUS	673 bp mRNA linear EST 21-APR-2004
DEFINITION	UI-M-HB0-cov-e-16-0-UI-r1 NIH BMAP_HB0 Mus musculus cDNA clone
IMAGE:30649359	5', mRNA sequence.
CN459710	
ACCESSION	CN459710.1
VERSION	GI:46465436
KEYWORDS	EST.
SOURCE	Mus musculus (house mouse)
ORGANISM	Mus musculus
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

REFERENCE

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Straubeberg, Ph.D.  
Email: [scapbe-remail.nih.gov](mailto:scapbe-remail.nih.gov)

Tissue Procurement: Dr. James Lin University of Iowa  
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa  
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
Clone Distribution: Distribution information can be found at  
<http://genome.uiowa.edu/distribution/mousefl.html>  
This clone was contributed by the Brain Molecular Anatomy Project (BMAP)

Seq primer: pYX-5.

FEATURES

Location/Qualifiers  
1..673  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="C57BL/6"  
/db\_xref="taxon:10090"  
/clone="IMAGE:30649359"  
/tissue\_type="whole eye"  
/dev\_stage="embryo 12.5,13.5,14.5 dpc"  
/lab\_host="DH10B (T1 phage resistant)"  
/clone\_lib="NIH BMAP HB0"  
/note="Organ: Eye; Vector: pYX- Asc; Site 1: Ecor I; Site 2: Not I; The library was constructed according to Bernaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with Ecor I adaptor, digested with NotI and then cloned directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is TTTATGAGT. This library was created for the University Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH)."

ORIGIN

Query Match	62.7%;	Score 613.2;	DB 7;	Length 673;
Best Local Similarity	95.0%;	Pred. No. 2.9e-154;	Indels 0;	Gaps 0;
Matches 633;	Conservative 0;	Mismatches 33;	Indels 0;	Gaps 0;
Qy	70	TTTGGGAAAGTTATTTTGGTTTCGAGAGAGGCAAGTGGAAATACTATGCTATGAAGATT	129	
Db	8	TTTGGGAAAGTTATTTTGGTTTCGAGAGAGGCAAGTGGAAATACTATGCTATGAAGATT	67	
Qy	130	CTGAAGAAAGAGTCATTATTGCAAGGATGAAGTGGCACACACTCTAACTGAAAGCAGA	189	
Db	68	CTGAAGAAAGAGTCATTATTGCAAGGATGAAGTGGCACACACTCTTACTGAAAGCAGA	127	
Qy	190	GTATTAAGAAACACATAGACATCCCTTTTAAATCTCTTGAATAATTCCTTCAGACAAAA	249	
Db	128	GTACTAAAGAACACACAGACATCCATTTTAAATCTCTTGAATAATTCCTTCAGACAAAA	187	
Qy	250	GACCGTTTGTGTTTGTGATGGAATATGTTAAATGGGCGGAGCTGTTTTTCCATTGTCG	309	
Db	188	GACCGTTTGTGTTTGTGATGGAATATGTTAAATGGGCGGAGCTGTTTTTCCATTGTCG	247	
Qy	310	AGAGAGCGGGTGTCTCTGAGGACCGCACACGCTTTTCTATGTCGAGAAATGTCCTCTGCC	369	
Db	248	AGAGAGCGAGTGTCTCTGAGGACCGCACACGCTTTTCTATGTCGAGAAATGTCCTCTGCC	307	
Qy	370	TTGACTATCTACATTCGGAAGAGATTGTGTACCGTGTATCTCAAGTTGGAGAAATCTAATG	429	
Db	308	TTGACTATCTACATTCGGAAGAGATTGTGTACCGTGTATCTCAAGTTGGAGAAATCTAATG	367	
Qy	430	CTGACAAAGATGGCCACATATAAATATACATTTTGGACTTTTGGCAAGAGGATCACA	489	

Db 368 CTAGATAAGGATGCCCATATAAAATTTACGAGTTTTCGGCTTTTGCATGAAGGAGATCACA 427

QY 490 GATCAGCCACCATGAAGACATCTGTGGCACTCCAGAATATCTGGCACCAGAGGTCTTA 549

Db 428 GATGACGCTACCATGAAGACATCTGTGGCACCAGAGATCTGGCACCAGAGGTATTA 487

QY 550 GAAGATAATGACTATGCGCGAGCAGTAGACTGTGGGCGCTTAGGGGTTGTCTGTATGAA 609

Db 488 GAAGATAATGACTATGCGCGAGCAGTAGACTGTGGGCGCTTAGGGGTTGTCTGTATGAA 547

QY 610 ATGATGTGTGGAGGTACCTTTCTACACCCAGACCATGAGAACTTTTGAATTAATA 669

Db 548 ATGATGTGTGGAGGTGCGCTTTCTACACCCAGGATCATGAGAACTCTTTGAATTAATA 607

QY 670 TTAATGAAGACATTAATTTCTCGAACACTCTCTTCAGATGCAAAATCATTTGCTTTCA 729

Db 608 CTAATGAGACATTAATTTCCCGGACACTCTCTTCAGATGCAAAATCATTTGCTTTCA 667

QY 730 GGGCTC 735

Db 668 GGGCTC 673

RESULT 12

CF741213

LOCUS

DEFINITION

UI-M-GHO-cll-c-19-0-UI.r1 NIH BMAP\_GHO Mus musculus cDNA clone

IMAGE:30618210 5', mRNA sequence.

CF741213

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Mus musculus (house mouse)

Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.

1 (bases 1 to 691)

NIH-MGC <http://mgc.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: [cgapso-remail.nih.gov](mailto:cgapso-remail.nih.gov)

Tissue Procurement: Dr. James Lin, University of Iowa

cDNA Library preparation: Dr. M. Bento Soares, University of Iowa

cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Distribution information can be found at <http://genome.uiowa.edu/distribution/mousefl.html>

This clone was contributed by the Brain Molecular Anatomy Project (BMAP)

## FEATURES

source

Location/Qualifiers

1..691

/organism="Mus musculus"

/mol\_type="mRNA"

/strain="C57BL/6"

/db\_xref="taxon:10090"

/clone="IMAGE:30618210"

/tissue\_type="whole brain"

/dev\_stage="1, 5, and 15 days newborn"

/lab\_host="DH10B (T1 phage resistant)"

/clone\_lib="NIH BMAP\_GHO"

/note="Organ: Brain; Vector: pYX-Asc; Site: 1: EcoR I; Site 2: Not I; The library was constructed according to Bonaldi, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with NotI and then cloned directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is CGAAGTGAAT. This library was created for the University

Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator."

## ORIGIN

Query Match 61.7%; Score 603.6; DB 6; Length 691;

Best Local Similarity 94.6%; Pred. No. 1.1e-151;

Matches 646; Conservative 0; Mismatches 35; Indels 2; Gaps 2;

QY 1 TCTACACCCCATCATATAAAGAAAGACATGAATGATTTTGACTATTTTGAAACTACTAGGT 60

Db 11 TCTACACCCCATCATATAAAGAAAGACATGAATGATTTTGACTATTTTGAAACTACTAGGT 70

QY 61 AAAGGCACATTTTGGGAAAGTTATTTTGGTTCGAGAGAGGCAAGTGGGAAATATCTATGCT 120

Db 71 AAAGG-ACITTTGGGAAAGTTATTTTGGTTCGAGAGAGGCAAGTGGGAAATATCTATGCT 129

QY 121 ATGAAGATTCCTGAAGAAAGAGTCAATTTATTTGCAAGGATGAAGTGGGCACACACTTAAC 180

Db 130 ATGAAGATTCCTGAAGAAAGAGTCAATTTATTTGCAAGGATGAAGTGGGCACACACTTTACT 189

QY 181 GAAAGCAGAGTATTAAGAAACACTAGACATCCCTTTTAAATCTCTTGAATATATCTCTTC 240

Db 190 GAAAGCAGAGTACTAAAGAAACACACAGACATCCATTTTAAATCTCTTGAATATATCTCTTC 249

QY 241 CAGACAAAGACCGTTTGTCTTTTGTGATGGAATATGTTAATGGGGCGAGCTGTTTTTC 300

Db 250 CAGACAAAGACCGTTTGTCTTTTGTGATGGAATATGTTAATGGGGCGAGCTGTTTTTC 309

QY 301 CATTTGTGAGAGAGCGGGTGTCTCTGAGGACCGCACACGTTTCTATGTTGCAGAAAT 360

Db 310 CATTTGTGAGAGAGCGAGTGTCTCTGAGGACCGCACACGTTTCTATGTTGCAGAAAT 369

QY 361 GTCTCTGCTTGAACACTCTACATTCGGGAAAGATGTTGTACCGTATCTCAAGTTGCGAG 420

Db 370 GTCTCTGCTTGAACACTCTACATTCGGGAAAGATGTTGTACCGTATCTCAAGTTGCGAG 429

QY 421 AATCTAATGCTGCACAAAGATGGCCACATATAAATTTACAGATTTTGACATTTTGCAAGAA 480

Db 430 AATTTGATGCTAGATGAAGATGGCCATATAAATTTACGGATTTTGGGCTTTGCAAGAA 489

QY 481 GGGATCACAGATCCAGCCACCATGAAGACATTCGTGGGCACTCCAGAAATATCTGGCACCA 540

Db 490 GGGATCACAGATCCAGCTACCATGAAGACATTCGTGGGCACTCCAGAGTAGTACCTGGCACCA 549

QY 541 GAGGTGTAGAACATAATGACTATGGCCGAGCAGTAGACTGGTGGGCGCTTAGGGGTTGTC 600

Db 550 GAGGTATTAGAAGATAATGACTATGGCCGAGCGCTGGACTGGTGGGCGCTTAGGGGTTGTC 609

QY 601 ATGTATGAAATGATGTGGGAGTTACCTTTCTACAAACAGGACCATGAGAACTTTT 660

Db 610 ATGTATGAAATGATGTGGGAGTTGCTTCTACAAACAGGATCATGAG-AACTCTTT 668

QY 661 GAATTAATTAATTAATGAAGACAT 683

Db 669 GNAATTATACTAATGAAGACAT 691

## RESULT 13

BU055259

LOCUS

DEFINITION

UI-M-FOO-bzp-j-23-0-UI.r1 NIH BMAP\_FOO Mus musculus cDNA clone

IMAGE:6405622 5', mRNA sequence.

BU055259

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Mus musculus (house mouse)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.

1 (bases 1 to 675)

REFERENCE

BU055259 675 bp mRNA linear EST 26-AUG-2002

UI-M-FOO-bzp-j-23-0-UI.r1 NIH BMAP\_FOO Mus musculus cDNA clone

IMAGE:6405622 5', mRNA sequence.

BU055259 1 GI:22495349

**AUTHORS** NIH-MGC <http://mgc.nci.nih.gov/>  
**TITLE** National Institutes of Health, Mammalian Gene Collection (MGC)  
**JOURNAL** Unpublished (1999)  
**COMMENT** Contact: Robert Strausberg, Ph.D.  
 Email: [cgabbs-remail.nih.gov](mailto:cgabbs-remail.nih.gov)  
 Tissue procurement: Dr. Jim Lin, University of Iowa  
 cDNA Library preparation: Dr. M. Bento Soares, University of Iowa  
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
 Clone Distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
 This clone was contributed by the Brain Molecular Anatomy Project  
 (BMAP)  
**FEATURES** Seq primer: pYX-5.  
 Location/Qualifiers  
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 /organism="Mus musculus"  
 /mol\_type="mRNA"  
 /strain="C57BL/6"  
 /db\_xref="taxon:10090"  
 /clone="IMAGE:6405622"  
 /tissue\_type="whole brain"  
 /dev\_stage="embryo 12.5dpc"  
 /lab\_host="DH10B (T1 phage resistant)"  
 /clone\_lib="NIH-BMAP\_F00"  
 /note="Organ: Brain; Vector: pYX-Asc; Site\_1: EcoR I;  
 Site\_2: Not I; The library was constructed according  
 Bernaldo, Lennon and Soares, Genome Research, 6:791-806,  
 1996. Denatured RNA was size fractionated on a 1% agarose  
 gel. First strand cDNA synthesis was primed with oligo-dT  
 primer containing a Not I site. Double strand cDNA was  
 size selected according to mRNA size fraction, ligated  
 with EcoR I adaptor, digested with NotI and then cloned  
 directionally into pYX-Asc vector. The library tag  
 sequence located between the Not I site and the polyA tail  
 is TCAGAGAGCC. This library was created for the University  
 Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the  
 Developing Mouse Nervous System', supported by National  
 Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,  
 program coordinator."

## ORIGIN

Query Match 61.2%; Score 598.8; DB 5; Length 675;  
 Best Local Similarity 94.8%; Pred. No. 2.2e-150;  
 Matches 640; Conservative 0; Mismatches 33;  
 Indels 2; Gaps 2;

Qy 1 TCTACACCCATCAATAAGAAAGCAATGATGATTTTGACTATTTCGAACACTAGGT 60  
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 Db 3 TCTACACCCATCAATAAGAAAGCAATGATGATTTTGACTATTTCGAACACTAGGT 62  
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Qy 61 AAAGGCACCTTTTGGAAAGTTATTTTGGTTTCGAGAGAGGCAAGTGGAAATACATGCT 120  
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 Db 63 AAAGGCACCTTTTGGAAA-TTATTTTGGTTTCGAGAGAGGCAAGTGGAAATACATGCT 121  
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Qy 121 ATGAAGATCTGAAGAAAGAGTCAATTATGCAAAAGGATGAAGTGGCCACACCTTAAT 180  
 |||||  
 Db 122 ATGAAGATCTGAAGAAAGAGTCAATTATGCAAAAGGATGAAGTGGCCACACCTTAAT 181  
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Qy 181 GAAAGCAGATTAATAAGACACATGACATCCCTTTTAAACATCCCTTGAATATTCCTTC 240  
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 Db 182 GAAAGCAGATTAATAAGACACACACGACATCCATTTTAAACATCCCTTGAATATTCCTTC 241  
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Qy 241 CAGACAAAAGACCGTTTGTGTTTGTGATGGAATATGTTAATGGGGCGAGCTGTTTTTC 300  
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 Db 242 CAGACAAAAGACCGTTTGTGTTTGTGATGGAATATGTTAATGGGGCGAGCTGTTTTTC 301  
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Qy 301 CATTTGTGAGAGACGGGTGTTCTCTGAGGACCGCACACAGTTTCTATGGTGCAGAAAT 360  
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 Db 302 CATTTGTGAGAGACGGAGTGTCTCTGAGGACCGCACACAGTTTCTATGGTGCAGAAAT 361  
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Qy 361 GTCTCTGCTTGGACTATCTACATTCGGAAAGATTGTGTACCGTGATCTCAAGTTGGAG 420  
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Db 362 GTCTCTGCTTGGACTATCTACATTCGGAAGATTGTGTACCGTGATCTCAAGTTGGAG 421  
 Qy 421 AATCTAATGCTGGACAAAGATGGCCACATAAAATTCAGATTTTGGACTTTGCAAGAA 480  
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 Db 422 AATTTGATGCTAGATAAGATGGCCATATAAAATTCAGGATTTTGGGCTTTGCAAGAA 481  
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 Qy 481 GGGATCAGATGCGAGCCACCATGAAGACATCTGTGGCACTCCAGATATCTGGCACA 540  
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 Db 482 GGGATCAGATGCGAGCTTACCATGAAGACATCTGTGGCACTCCAGATATCTGGCACA 541  
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 Qy 541 GAGGTGTTAGAAAGATAATGACTATATGGCGAGCGTGTGGGCTTGGGCTTGTGTC 600  
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 Db 542 GAGGTATTAGAAAGATAATGACTATATGGCGAGCGTGTGGGCTTGTGTC 601  
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Qy 601 ATGTATGAATGATGTGGGAGGTATACCTTTTCTACACAGGACCATGAGAAATTTT 660  
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 Db 602 ATGTATGAATGATGTGGAGGTTGCTTTCTACACAGGACCATGAG-AACTCTTT 660  
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Qy 661 GAATTAATATTAATG 675  
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 Db 661 GAATTAATATTAATG 675  
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RESULT 14  
 BU790247/c

LOCUS BU790247  
 DEFINITION in52e10.x1 HR85 islet Homo sapiens cDNA clone IMAGE:6125683 3',  
 similar to TR:Q9Y243 Q9Y243 PROTEIN KINASE B GAMMA. ; mRNA  
 sequence.

## ACCESSION

BU790247

## VERSION

BU790247.1 GI:23840478

## KEYWORDS

EST.

## SOURCE

Homo sapiens (human)

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homnidae; Homo.

## REFERENCE

1 (bases 1 to 594)

## AUTHORS

Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,  
 Lemishka,I., Searce,M., Pape,D., Wylie,T., Martin,J., Clifton,S.,  
 Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A.,  
 Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J.,  
 Cardenas,M., Gibbons,M., McCann,R., Cole,R., Tsagarishvili,R.,  
 Williams,T., Jackson,Y. and Bowers,Y.

## TITLE

Unpublished (2000)

## JOURNAL

COMMENT

Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue  
 Endocrine Pancreas Consortium  
 Harvard University, Howard Hughes Medical Institute  
 Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,  
 MA 02138

Tel: 617-495-1812

Fax: 617-495-8557

Email: [dmelton@bioh.harvard.edu](mailto:dmelton@bioh.harvard.edu)

Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:  
 Washington University Genome Sequencing Center For information on  
 obtaining a clone please contact: Dr. Hiroshi Inoue  
 (hinoue@im.wustl.edu)

Seq primer: -40UP from Gibco

High quality sequence stop: 439.

## FEATURES

## source

1..594

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:6125683"

/tissue\_type="Purified pancreatic islet"

/lab\_host="DH10B"

/clone\_lib="HR85 islet"

/note="Organ: Pancreas; Vector: pBluescript SK(-); Site\_1:  
 NotI; Site\_2: XhoI; cDNA made by oligo-dT priming.  
 Size-selected on agarose gel. Average insert size ~1kb. 5'  
 XhoI site was destroyed after directional cloning.

Amplified once. Contact information: Hiroshi Inoue, MD, Metabolism Div. (Alan Permutt Lab), Washington University School of Medicine, Box 8127, 660 South Euclid Ave., St. Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel: 314-362-1916, Fax: 314-747-2692."

## ORIGIN

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Query Match      60.7%; Score 594; DB 5; Length 594;
Best Local Similarity 100.0%; Pred. No. 4.3e-149;
Matches 594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 426 AATGCTCGACAAAGATGCCACATATAAAATACAGATTTTGGACTTTGCCAAGNAGGGAT 485
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Qy 486 CACAGATGCAGCCACCACTGAAGACATTTCTGTGGCACTCCAGAAATATCTGGCACCAGAGGT 545
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Qy 546 GTTAGAAGATAATGACTATGCGCAGCAGTAGACTGTGTGGGGCTAGGGGTGTGTCATGTA 605
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Qy 606 TGAATCATGTGTGGAGGTACCTTTCTACACCAGGACCATCAGAACTTTTGAATTT 665
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Qy 726 TTCAGGCTCTTGATAAAGGATCAAAATAAACCGCTTGTGGAGGACCATGATGCAAA 785
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Qy 846 GCTTGTACCTCTTTTAAACCTCAAGTAAACATCTGAGACAGATACTAGATATTTGATGA 905
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Qy 906 AGAATTTACAGCTCAGACTATTACAATAACACCACTGAAATAATATGATGAGGA 959
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## RESULT 15

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CN526605
LOCUS      710 bp mRNA linear EST 29-APR-2004
DEFINITION UT-M-HNO-cou-n-06-0-UI.r1 NIH BMAP_HNO Mus musculus cDNA clone
IMAGE:30650717 5', mRNA sequence.

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CN526605
VERSION    1
KEYWORDS   EST.
SOURCE     Mus musculus (house mouse)

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## ORGANISM

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Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
1 (bases 1 to 710)

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## REFERENCE

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AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
          Email: cgapbs-remail.nih.gov
          Tissue Procurement: Dr. James Lin University of Iowa
          cDNA Library preparation: Dr. M. Bento Soares, University of Iowa

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cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Distribution information can be found at <http://genome.uiowa.edu/distribution/mousefl.html> This clone was contributed by the Brain Molecular Anatomy Project (BMAP)

Seq primer: pYX-5.

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Location/Qualifiers
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/clone="IMAGE:30650717"
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/lab_host="DH10B (T1 phage resistant)"
/clone_lib="NIH_BMAP_HNO"
/notes="Organ: Head; Vector: pYX-Asc; Site 1: Ecor I; Site 2: Not I; The library was constructed according BonaIdo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with Ecor I adaptor, digested with NotI and then cloned directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is CGAAGCTGAAT. This library was created for the University Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH)."
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## ORIGIN

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Query Match      60.7%; Score 593.8; DB 7; Length 710;
Best Local Similarity 92.8%; Pred. No. 5.1e-149;
Matches 655; Conservative 0; Mismatches 48; Indels 3; Gaps 3;

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Db 61 CACACGTTTCTATGTTGCAGAAAATTTGCTCTGCTTGGACTATCTACATTTCCGGAAGAT 120

Qy 396 TGTGTACCGTGATCTCAAGTTGGAGAAATTTGATGCTAGATAAGGATGCCATATAAAAT 455
Db 121 TGTGTACCGTGATCTCAAGTTGGAGAAATTTGATGCTAGATAAGGATGCCATATAAAAT 180

Qy 456 TACAGATTTTGGACTTTGCAAGAAGGGATCACAGATGCAGCCACCACCATGAAGACATTTCTG 515
Db 181 TACGGATTTTGGGCTTTGCAAGAAGGGATCACAGATGCAGCTACCATGAAGACATTTCTG 240

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661 AACACCACTGANAAGTATGACGACGCGCATGGCAGCGCATGGAC 706
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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM nucleic - nucleic search, using sw model

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11190.196 Million cell updates/sec

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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues  
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Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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2: gb\_in.\*  
3: gb\_env.\*  
4: gb\_om.\*  
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6: gb\_pat.\*  
7: gb\_ph.\*  
8: gb\_pri.\*  
9: gb\_ro.\*  
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14: gb\_hcg.\*  
15: gb\_pl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	978	100.0	1436	6	AX026530 Sequence
3	978	100.0	1440	6	BD142211 Method fo
4	978	100.0	1440	11	AY335691 Synthetic
5	978	100.0	1440	11	AY893474 Synthetic
6	978	100.0	1440	11	AY893919 Synthetic
7	978	100.0	1445	8	BC020479 Homo sapi
8	978	100.0	1547	6	BD251226 Human Akt
9	978	100.0	1547	6	AR593589 Sequence
10	978	100.0	1547	6	AX026529 Sequence
11	978	100.0	1547	8	HS245709 Homo sapi
12	978	100.0	1651	6	CQ714620 Sequence
13	978	100.0	1706	8	AF085234 Homo sapi
14	978	100.0	1708	8	AF124141 Homo sapi
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26	584.8	59.8	1808	5	AF317656 Xenopus l
27	570.6	58.3	4181	5	BC072041 Xenopus l
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29	561.2	57.4	1440	5	AY056465 Danio rer
30	527	53.9	1741	9	MMU22445 Mus musculu
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ACCESSION	BD251227.1	GI:33060997				
VERSION	JP 2002535964-A/2.					
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SOURCE	Homo sapiens (human)					
ORGANISM	Homo sapiens					

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 1436)  
AUTHORS Masure,S.L.J. and Richardson,A.  
TITLE Human Akt-3  
JOURNAL Patent: JP 2002535964-A 2 29-OCT-2002;  
JANSEN PHARMACEUTICA NV  
COMMENT OS Homo sapiens (human)  
PN JP 2002535964-A/2  
PD 29-OCT-2002  
PF 17-DEC-1999 JP 2000589669  
PR 22-DEC-1998 GB 9828375.7  
PI STEFAN LEO JOZEF MASURE,ALAN RICHARDSON

PC	C12N15/09,A61K31/713,A61K38/53,A61K39/395,A61K39/395,A61K48/00, PC
A61P35/00,	
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PC	12,C12Q1/02,
PC	C12Q1/48,G01N33/15,G01N33/50,G01N33/53,G01N33/566/C12P21/08,
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Hominiidae; Homo.									
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1 Masure,S.L. and Richardson,A.									
AUTHORS									
TITLE									
JOURNAL									
Patent: WO 0037613-A 2 29-JUN-2000;									
MASURE STEFAN LEO JOZEF (BE) ; RICHARDSON ALAN (BE) ; JANSSEN									
PHARMACEUTICA NV (BE)									
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Qy	1	TCTACAACCCATCATAAAGAAAGACAAATGAATGATTTTGACATATTGAACTACTAGGT	60						
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SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.		
AUTHORS	Tsuruo T., Fujita N. and Sato S.		
TITLE	Method for controlling apoptosis and polypeptide controlling		
JOURNAL	Patent: WO 0215925-A 5 28-FEB-2002;		
COMMENT	KYOWA HAKKO KOGYO CO LTD, TAKASHI TSURUO, NAOYA FUJITA, SAORI SATO		
	OS Homo sapiens (human)		
	PN WO 0215925-A/5		
	PD 28-FEB-2002		
	PP 22-AUG-2001	WO 2001JP007179	
	PR 22-AUG-2000	JP 00P 251529	
	PI TAKASHI TSURUO, NAOYA FUJITA, SAORI SATO		
	PC A61K38/17, A61K38/45, A61K39/395, A61K45/00, A61P43/00, A61P3/08,		
	PC A61P35/00,		
	PC A61P43/00, C07K7/04, C07K14/47, C07K16/18, C12N1/15, C12N1/19 PC		
	C12N1/21, C12N5/10,		
	PC C12P21/02, C12N15/09, G01N33/50, G01N33/15, G01N33/566, G01N33/68		
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	PH Key	Location/Qualifiers	
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Best Local Similarity	100.0%;	Pred. No. 4.1e-206;	
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		0; Gaps	0;
QY	1	TCTACAACCCATCAATAAGAAAGACAATGAATGATTTTGACTATTGTAACCTACTAGGT	60
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QY	61	AAAGSCATTTTGGGAAAGTTATTTTGGTTCCAGAGAAAGGCAAGTGGAAAAATACTATGCT	120
Db	466	AAAGSCATTTTGGGAAAGTTATTTTGGTTCCAGAGAAAGGCAAGTGGAAAAATACTATGCT	525
QY	121	ATGAGATTTCTGAAGAAAGAGTCAATTATTCGAAAGGATGAAGTGGCAGACACTCTAACT	180
Db	526	ATGAGATTTCTGAAGAAAGAGTCAATTATTCGAAAGGATGAAGTGGCAGACACTCTAACT	585
QY	181	GAAAGCAGAGTATTAAAGAAACACATAGACATCCCTTTTAAACATCCTTGAATATTCCTTC	240
Db	586	GAAAGCAGAGTATTAAAGAAACACATAGACATCCCTTTTAAACATCCTTGAATATTCCTTC	645
QY	241	CAGACAAAAGACCGTTTGTGTTTGTGATGGAATATGTTTAATGGGGGGGAGCTGTTTTC	300
Db	646	CAGACAAAAGACCGTTTGTGTTTGTGATGGAATATGTTTAATGGGGGGGAGCTGTTTTC	705
QY	301	CATTTGTCGAGAGAGCGGTTCTCTGAGAGACCGCACACAGTTTCTATGGTGCAGAAATT	360
Db	706	CATTTGTCGAGAGAGCGGTTCTCTGAGAGACCGCACACAGTTTCTATGGTGCAGAAATT	765
QY	361	GTCTCTGCTTGGACTATCTACATTCGGAAGATTTGTATCCGTTGATCTCAAGTTGGAG	420
Db	766	GTCTCTGCTTGGACTATCTACATTCGGAAGATTTGTATCCGTTGATCTCAAGTTGGAG	825
QY	421	AATCTAATGCTGGCAAAAGATGGCCACATATAAAATTCACAGATTTTGGACTTTGCAAGNA	480
Db	826	AATCTAATGCTGGCAAAAGATGGCCACATATAAAATTCACAGATTTTGGACTTTGCAAGNA	885
QY	481	GGGATCACAGATGTCAGCCACCATGAAGACATTTCTGTGCACCTCCAGAAATATCTGCACCA	540
Db	886	GGGATCACAGATGTCAGCCACCATGAAGACATTTCTGTGCACCTCCAGAAATATCTGCACCA	945
QY	541	GAGGTGTTAGAAGATAATGACTATGCGCCGAGCAGTAGACTTGTGGGGCCTAGGGTTGTC	600
Db	946	GAGGTGTTAGAAGATAATGACTATGCGCCGAGCAGTAGACTTGTGGGGCCTAGGGTTGTC	1005
QY	601	ATGTAATAATGATGTGGAGGTTTACCTTTCTACAACAGGACCATGAGAAACTTTT	660
Db	1006	ATGTAATAATGATGTGGAGGTTTACCTTTCTACAACAGGACCATGAGAAACTTTT	1065
QY	661	GAATTAATTAATGGAAGACATTTAAATTTCTCCGAAACACTCTCTTCAGATGCAAAATCA	720
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Db	1126	TTGCTTTTCAGGCTCTTGATTAAGGATCCAAATAAACGCTTGGTGGAGCCAGATGAT	1185
QY	781	GCAAAAGAAATTAATGAGACACAGTTTCTCTCTGAGATTAACCTGGCAAGATGTATATGAT	840
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QY	841	AAAAAGCTTGTAACCTCTTTAAACCTCAAGTAAACATCTGAGACAGATAGATATTTT	900
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Db	1366	GGTATGGACTGCATGGAC	1383
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LOCUS	AY335691	1440 bp	mRNA linear SYN 08-JUN-2005
DEFINITION	Synthetic construct Homo sapiens v-akt murine thymoma viral		
ACCESSION	AY335691		
VERSION	AY335691.1	GI:33304020	

KEYWORDS	FLI_CDNA.
SOURCE	synthetic construct
ORGANISM	other sequences: artificial sequences.
REFERENCE	1 (bases 1 to 1440)
AUTHORS	Park,J., Hu,Y., Murthy,T.V.S., Vannberg,F., Shen,B., Rolfs,A., Hutti,J.E., Cantley,L.C., LaBaer,J., Harlow,E. and Brizuela,L. Building a human kinase gene repository: Bioinformatics, molecular cloning, and functional validation
TITLE	Proc. Natl. Acad. Sci. U.S.A. 102 (23), 8114-8119 (2005)
JOURNAL	15928075
PUBMED	2 (bases 1 to 1440)
REFERENCE	Park,J., Rolfs,A., Hu,Y., Shen,B., Vannberg,F., Moreira,D., Kelley,T., Zuo,D., Raphael,J., Baqui,M., Jepson,D., Harlow,E., LaBaer,J. and Brizuela,L.
AUTHORS	Direct Submission
TITLE	Submitted (02-JUL-2003) Biological Chemistry and Molecular Pharmacology, Harvard Institute of Proteomics, 320 Charles St., Cambridge, MA 02141-2023, USA
JOURNAL	This CDS clone is a part of a collection of human full-length expression clones generated by Harvard Institute of Proteomics. Each CDS has been cloned without stop-codon (to allow fusion with C-terminal tag). The CDS has been directionally cloned using BD In-Fusion(TM) cloning system between the Sali and HindIII sites of the pDNR-Dual vector. Additional sequences in the clone: 'ACC' after Sali site and before 'ATG' to provide Kozak consensus sequence; 'GG' after last codon and before HindIII site to maintain reading frame.
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ORIGIN

Query Match	100.0%; Score 978; DB 11; Length 1440;
Best Local Similarity	100.0%; Pred. No. 4.1e-206;
Matches 978; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
Qy	1 TCTACACCCATATAAAGAACACATGAATGATTTTGACTATTTCGAACACTACTAGGT 60
Db	406 TCTACACCCATATAAAGAACACATGAATGATTTTGACTATTTCGAACACTACTAGGT 465
Qy	61 AAAGGCATTTTGGGAAAGTTATTATTTTGGTCGAGAGAGGCAAGTGGGAAATATACTATGCT 120
Db	466 AAAGGCATTTTGGGAAAGTTATTATTTGGTCGAGAGAGGCAAGTGGGAAATATACTATGCT 525
Qy	121 ATGAAGATTCTGAAGAAAGATGATTAATTCGAAAGGATGAAGTGGGCACACACTCTTAAC 180

Db	526 ATGAAGATTCTGAAGAAAGATGATTAATTCGAAAGGATGAAGTGGGCACACACTCTTAAC 585
Qy	181 GAAAGCAGAGTATTAAAGAAACACTAGACATCCCTTTTAAACATCCTTTGAAATATTTCCTTC 240
Db	586 GAAAGCAGAGTATTAAAGAAACACTAGACATCCCTTTTAAACATCCTTTGAAATATTTCCTTC 645
Qy	241 CAGACAAAACACCGTTTGTGTTTGTGATGGAATATGTTAATGGGCGAGCTGTTTTTC 300
Db	646 CAGACAAAACACCGTTTGTGTTTGTGATGGAATATGTTAATGGGCGAGCTGTTTTTC 705
Qy	301 CATTTGTGAGAGAGCGGGTGTCTCTGAGGACCGCACACAGTTTCTATGTCGAGAAATT 360
Db	706 CATTTGTGAGAGAGCGGGTGTCTCTGAGGACCGCACACAGTTTCTATGTCGAGAAATT 765
Qy	361 GTCTCTCCCTTGGACTACTACATTCGCGAAAGATTGTGTACCGTGTATCTCAAGTTGGAG 420
Db	766 GTCTCTCCCTTGGACTACTACATTCGCGAAAGATTGTGTACCGTGTATCTCAAGTTGGAG 825
Qy	421 AATCTAATGCTGGACAAAGATGGCCACATATAAAATTTACAGATTTTGGACATTTGCAAGAA 480
Db	826 AATCTAATGCTGGACAAAGATGGCCACATATAAAATTTACAGATTTTGGACATTTGCAAGAA 885
Qy	481 GGGATCACAGATGAGCAGCACCATGAAGACATTTCTGTGGCACTCCAGAAATATCTGGCACCA 540
Db	886 GGGATCACAGATGAGCAGCACCATGAAGACATTTCTGTGGCACTCCAGAAATATCTGGCACCA 945
Qy	541 GAGGTGTTAGAAGATATGACTATGGCCGAGCAGTAGACTGTGGGCGCTAGGGGTTGTC 600
Db	946 GAGGTGTTAGAAGATATGACTATGGCCGAGCAGTAGACTGTGGGCGCTAGGGGTTGTC 1005
Qy	601 ATGTATGAAATGATGTGTGGAGGTTACCTTTCTACAACGAGGACCATGAGAAACTTTTT 660
Db	1006 ATGTATGAAATGATGTGTGGAGGTTACCTTTCTACAACGAGGACCATGAGAAACTTTTT 1065
Qy	661 GAATTAATATTAATGGAAGACATTAATTTCTTCGAAACACTCTTTCAGATGCAAAATCA 720
Db	1066 GAATTAATATTAATGGAAGACATTAATTTCTTCGAAACACTCTTTCAGATGCAAAATCA 1125
Qy	721 TTGCTTTTCAGGGCTCTTGATAAAGGATCCAAATAAAGCCCTTGGTGAGGACCAAGATGAT 780
Db	1126 TTGCTTTTCAGGGCTCTTGATAAAGGATCCAAATAAAGCCCTTGGTGAGGACCAAGATGAT 1185
Qy	781 GCAAAAGAAATATGAGACACAGTTTCTTCTGTGGAGTAAACTGGCAAGATGTATATGAT 840
Db	1186 GCAAAAGAAATATGAGACACAGTTTCTTCTGTGGAGTAAACTGGCAAGATGTATATGAT 1245
Qy	841 AAAAGCTTGTACCTCTCTTTTAAACCTCAAGTAAACATCTGAGACAGATAGTATATTT 900
Db	1246 AAAAGCTTGTACCTCTCTTTTAAACCTCAAGTAAACATCTGAGACAGATAGTATATTT 1305
Qy	901 GATGAAGAAATTTACAGCTCAGACTATTACAAATACACCACTGAAAAATATGATGAGGAT 960
Db	1306 GATGAAGAAATTTACAGCTCAGACTATTACAAATACACCACTGAAAAATATGATGAGGAT 1365
Qy	961 GGTATGACCTGTCATGGAC 978
Db	1366 GGTATGACCTGTCATGGAC 1383
RESULT 5	
AY893474	
LOCUS	AY893474 1440 bp mRNA linear SYN 16-MAR-2005
DEFINITION	Synthetic construct Homo sapiens clone FLH127839.01X v-akt murine thymoma viral oncogene-like 3 (AKT3) mRNA, complete cds.
ACCESSION	AY893474
VERSION	AY893474.1 GI:60819745
KEYWORDS	Human ORF Project
SOURCE	synthetic construct
ORGANISM	synthetic construct
REFERENCE	1 (bases 1 to 1440)
AUTHORS	Hines,L., Taron,B., Jepson,D., Moreira,D., Raphael,J., Shen,B., Halleck,A., Koundinya,M., Hu,Y., Zuo,D. and LaBaer,J.



COMMENT This CDS clone is a part of a collection of human full-length expression clones generated by Harvard Institute of Proteomics. This ORF clone has been cloned without stop-codon (to allow fusion with C-terminal tag). AttB recombination sites have been added to either end of the ORF and directionally cloned using the Gateway cloning system into pDONR 201. Additional sequences in the clone: 'ACC' before the 'ATG' (corresponding to ribosomal binding site and Kozak consensus sequences). Each clone is clonally isolated and full-length sequence-verified.

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ORIGIN

Query Match 100.0%; Score 978; DB 11; Length 1440;  
Best Local Similarity 100.0%; Pred. No. 4.1e-206;  
Matches 978; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 TCTCAACCCATCAATAAGAAAGACAAATGAATGATTTGACTATTTGAACTACTAGGT 60  
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Qy 406 TCTACACCCATCATAAAGAAAGACAAATGAATGATTTGACTATTTGAACTACTAGGT 465  
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Qy 61 AAAGGCACTTTGGGAAAGTATTTTGGTTTCGAGAGAGGCAAGTGGAAATATCTATGCT 120  
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Qy 466 AAAGGCACTTTGGGAAAGTATTTTGGTTTCGAGAGAGGCAAGTGGAAATATCTATGCT 525  
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RESULT 7  
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LOCUS Homo sapiens v-akt murine thymoma viral oncogene homolog 3 (protein  
DEFINITION kinase B, gamma), mRNA (cDNA clone IMAGE:3867931), partial cds.  
BC020479  
ACCESSION BC020479.1 GI:18042842  
VERSION  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
REFERENCE 1 (bases 1 to 1445)  
AUTHORS Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,  
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,  
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,  
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Heieh, F.,  
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,  
Scapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,  
Scherst, T.E., Brownstein, M.J., Ustin, T.B., Toshikiyuki, S.,  
Carinci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,  
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,  
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,  
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,  
Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,  
Fahney, J., Helton, E., Kettelman, M., Madan, A., Rodriguez, S.,  
Sanchez, A.G., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,  
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,  
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,  
Butterfield, Y.S., Krzywicki, M.I., Skalek, U., Smalls, D.E.,  
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.  
Mammalian Gene Collection Program Team  
Generation and initial analysis of more than 15,000 full-length  
TITLE

JOURNAL human and mouse cDNA sequences  
 PUBMED Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)  
 REFERENCE 12477932  
 2 (bases 1 to 1445)  
 AUTHORS NIH MGC Project  
 TITLE Direct Submission  
 JOURNAL Submitted (03-JAN-2002) National Institutes of Health, Mammalian  
 Gene Collection (MGC), Bethesda, MD 20892-2590, USA  
 NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
 CONTACT: MGC help desk  
 Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
 Tissue Procurement: ATCC  
 CDNA Library Preparation: Life Technologies, Inc.  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Baylor College of Medicine Human Genome  
 Sequencing Center  
 Center code: BCM-HGSC  
 Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>  
 Contact: [amg@bcm.tmc.edu](mailto:amg@bcm.tmc.edu)  
 Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H.,  
 Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,  
 A.N., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found  
 through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
 Series: IRAC Plate: 13 Row: h Column: 23  
 This clone was selected for full length sequencing because it  
 passed the following selection criteria: matched mRNA gi: 32307164.

## FEATURES

## source

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## ORIGIN

Query Match 100.0%; Score 978; DB 8; Length 1445;  
 Best Local Similarity 100.0%; Pred. No. 4.1e-206;  
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 DB 452 TCTAACCCATCAATAAGAAAGCAATGAATGATTTTGAATCTAGGT 511  
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QY 121 ATGAAGATTCTGAAGAAAGAAAGTCAATTATTCGAAAGGATGAAGTGGCACACACTCTAACT 180  
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RESULT 8  
 BD251226  
 LOCUS Human Akt-3.  
 DEFINITION BD251226.1  
 ACCESSION BD251226.1 GI:33060996  
 VERSION JP 2002535964-A/1.  
 KEYWORDS Homo sapiens (human)  
 SOURCE  
 ORGANISM Homo sapiens  
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

REFERENCE 1 (bases 1 to 1547)  
AUTHORS Masure,S.L.J. and Richardson,A.  
TITLE Human Akt-3  
JOURNAL Patent: JP 2002535964-A 1 29-OCT-2002;  
JANSSEN PHARMACEUTICA NV  
COMMENT OS Homo sapiens (human)  
PN JP 2002535964-A/1  
PD 29-OCT-2002  
PF 17-DEC-1999 JP 2000589669  
PR 22-DEC-1998 GB 9828375.7  
PI STEFAN LEO JOZEF MASURE,ALAN RICHARDSON  
PC C12N15/09,A61K31/713,A61K38/53,A61K39/395,A61K39/395,A61K48/00,PC A61P35/00,  
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PC C12Q1/48,G01N33/15,G01N33/50,G01N33/53,G01N33/566//C12P21/08,  
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Best Local Similarity 100.0%; Pred. No. 4.1e-206;  
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Db 1376 GGTATGAGCTGCATGGAC 1393  
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LOCUS AR593589 1547 bp DNA linear PAT 15-DEC-2004  
DEFINITION Sequence 1 from patent US 6809194.  
ACCESSION AR593589  
VERSION AR593589.1 GI:56642796  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 1547)  
AUTHORS Reinhard,C. and Jefferson,A.B.  
TITLE Akt3 inhibitors  
JOURNAL Patent: US 6809194-A 1 26-OCT-2004;  
Chiron Corporation; Emeryville, CA  
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ORIGIN  
Query Match 100.0%; Score 978; DB 6; Length 1547;  
Best Local Similarity 100.0%; Pred. No. 4.1e-206;  
Matches 978; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 TCTCAACCCATCATAAAGAAAGACAAATGAATGATTTTGACTATTTTGAACACTACTAGGT 60  
Db 416 TCTCAACCCATCATAAAGAAAGACAAATGAATGATTTTGACTATTTTGAACACTACTAGGT 475  
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Db 1376 GGTATGGACTGCATGGAC 1393

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RESULT 11

HSA245709 1547 bp mRNA linear PRI 15-APR-2005

LOCUS Homo sapiens mRNA for serine/threonine kinase Akt-3 (Akt3 gene).

DEFINITION AJ245709

ACCESSION AJ245709.1 GI:5804885

VERSION

KEYWORDS Akt-3; Akt3 gene.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

1

REFERENCE

AUTHORS Masure,S., Haefner,B., Wesselink,J.J., Hoefnagel,E., Mortier,E., Verhaegelt,P., Tuytelaars,A., Gordon,R. and Richardson,A.

TITLE Molecular cloning, expression and characterization of the human serine/threonine kinase Akt-3

JOURNAL Eur. J. Biochem. 265 (1), 353-360 (1999)

PUBMED 10491192

REFERENCE 2 (bases 1 to 1547)

AUTHORS Masure,S.L.

TITLE Direct Submission

JOURNAL Submitted (25-AUG-1999) Masure S.L., Biotechnology & High-Throughput Screening, Janssen Research Foundation, Turnhoutseweg 30, B-2340 Beerse, BELGIUM

COMMENT Phosphorylation at Thr305 and at Ser472 necessary for activation.

FEATURES

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11. .1450

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3'UTR

ORIGIN

Query Match 100.0%; Score 978; DB 8; Length 1547;

Best Local Similarity 100.0%; Pred. No. 4.1e-206;

Matches 978; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCTACACCCATCATAAAGAGAGACAATGAATGATTTTGGCTTTCGAGAGAGGCAAGTGGGCAATATCTATGCT 60

Db 416 TCTACACCCATCATAAAGAGAGACAATGAATGATTTTGGCTTTCGAGAGAGGCAAGTGGGCAATATCTATGCT 475

Qy 61 AAAGGCACTTTTGGGAAAGTTATTTTGGTTCGAGAGAGGCAAGTGGGCAATATCTATGCT 120

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Db 1376 GGTATGACTGCATGGAC 1393

RESULT 12

CQ714620

LOCUS

CQ714620 1651 bp DNA linear PAT 03-FEB-2004



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ACCESSION	CQ714620	Qy	721	TTGCTTTTTCAGGCTCTTGATAAAGGATCAATAAAGCGCTTTGGTGGAGGACAGATGAT	780
VERSION	CQ714620.1 GI:42275477	Db	1081	TTGCTTTTTCAGGCTCTTGATAAAGGATCAATAAAGCGCTTTGGTGGAGGACAGATGAT	1140
KEYWORDS	Homo sapiens (human)	Qy	781	GCAAGAAGAAATATGACACACAGATTTCTTCTCTGAGTAAACTGCGCAAGATCTATATGAT	840
SOURCE	Homo sapiens	Db	1141	GCAAGAAGAAATATGACACACAGATTTCTTCTCTGAGTAAACTGCGCAAGATCTATATGAT	1200
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.	Qy	841	AAAAAGCTTTGTACCTCCCTTTTAAACCTCAAGTAAACATCTGAGACAGATACTAGATATTTT	900
REFERENCE	Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.	Db	1201	AAAAAGCTTTGTACCTCCCTTTTAAACCTCAAGTAAACATCTGAGACAGATACTAGATATTTT	1260
AUTHORS	Kits, such as nucleic acid arrays, comprising a majority of humanexons or transcripts, for detecting expression and other uses thereof	Qy	901	GATGAAGAATTTACAGCTCAGCTCACTATTACAATAACACCACTGAAATAATATGATGAGAT	960
TITLE	Patent: WO 02068579-A 554 06-SEP-2002; PE Corporation (NY) (US)	Db	1261	GATGAAGAATTTACAGCTCAGCTCACTATTACAATAACACCACTGAAATAATATGATGAGAT	1320
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ORIGIN					
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Best Local Similarity	100.0%; Pred. No. 4e-206;				
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Db	541 GAAAGCAGAGTATTAAAGAACACTAGACATCCCTTTTAAACATCTCTGAAATATTCCTTC	AUTHORS	Li, X., Yu, L., Huang, H., Zhang, M., Zhao, Y., and Zhao, S.		
Qy	241 CAGACAAAAGACGTTTGTGTTTGTGATGGAATATGTTAATGGGGCGAGCTGTTTTC	TITLE	Cloning of a novel human cDNA, STK-2, which encodes a rat serine-threonine protein kinase (STK) homolog		
Db	601 CAGACAAAAGACGTTTGTGTTTGTGATGGAATATGTTAATGGGGCGAGCTGTTTTC	JOURNAL	Unpublished		
Qy	301 CATTTGTCGAGAGCGGGTGTCTCTGAGGACCGCACACGTTTCTATGTCGAGAAAT	AUTHORS	2 (bases 1 to 1706)		
Db	661 CATTTGTCGAGAGCGGGTGTCTCTGAGGACCGCACACGTTTCTATGTCGAGAAAT	TITLE	Zhao, Y.		
Qy	361 GTCTCTGCTTGGACTATCTACATTCGGAAGATTTGTACCGTGATCTCAAGTTGGAG	JOURNAL	Direct Submission		
Db	721 GTCTCTGCTTGGACTATCTACATTCGGAAGATTTGTACCGTGATCTCAAGTTGGAG	FEATURES	Submitted (22-AUG-1998) Zhao Y., Institute of Genetics, Fudan University, Lab of Human Gene Research, No. 220, Handan Road, Shanghai, People's Republic of China, 200433		
Qy	421 AATCTAATCTGGACAAAGATGCCACATAAATAATACAGATTTGGACTTTGCAAAAGAA	source	1..1706		
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ORIGIN					
Query Match	100.0%; Score 978; DB 8; Length 1706;				
Best Local Similarity	100.0%; Pred. No. 4e-206;				
Matches	978; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
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Db	453	TCTACAAACCCATATAAAGAAAGACAAATGAATGATTTTGGACTATTTTGAAACTACTAGGT	512
Qy	61	AAAGGCACCTTTTGGAAAGTTATTTTTGGTTCCAGAGAAGGCAAGTGGAAATATCTATGCT	120
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Qy	121	ATGAAGATTCTTGAAGAAAGAGTCAATTATTGTCAAAGGATGAAGTGGCACACACTCTAACT	180
Db	573	ATGAAGATTCTTGAAGAAAGAGTCAATTATTGTCAAAGGATGAAGTGGCACACACTCTAACT	632
Qy	181	GAAGAGCAGAGTATTAAAGAACACTAGACATCCCTTTTAAACATCCTTGAATATCTCCTTC	240
Db	633	GAAGAGCAGAGTATTAAAGAACACTAGACATCCCTTTTAAACATCCTTGAATATCTCCTTC	692
Qy	241	CAGACAAAAGACCGTTTGTGTTTGTGATGGAATATGTTAATGGGGCGAGCTGTTTTTC	300
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Qy	301	CATTGTGCGAGAGCGGGTGTCTCTGAGGACCGCACACGTTTCTATGGTGCAGAAATT	360
Db	753	CATTGTGCGAGAGCGGGTGTCTCTGAGGACCGCACACGTTTCTATGGTGCAGAAATT	812
Qy	361	GTCTCTGCTTGGACTATCTACATTCGGGAAAGATTGTGTACCGTGATCTCAAGTTGGAG	420
Db	813	GTCTCTGCTTGGACTATCTACATTCGGGAAAGATTGTGTACCGTGATCTCAAGTTGGAG	872
Qy	421	AATCTAATGCTGGCAAAAGATGGCCACATAAAATTACAGATTTTTGGACTTTGCAAGAA	480
Db	873	AATCTAATGCTGGCAAAAGATGGCCACATAAAATTACAGATTTTTGGACTTTGCAAGAA	932
Qy	481	GGGATCACAGATGCGAGCCACCATGAAGACATTTCTGTGGCACTCCAGAAATATCTGGCACCA	540
Db	933	GGGATCACAGATGCGAGCCACCATGAAGACATTTCTGTGGCACTCCAGAAATATCTGGCACCA	992
Qy	541	GAGGTGTTAGAAGATAATGACTATGGCCGACAGTAGACTGGTGGGGCTTAGGGGTTGTC	600
Db	993	GAGGTGTTAGAAGATAATGACTATGGCCGACAGTAGACTGGTGGGGCTTAGGGGTTGTC	1052
Qy	601	ATGTATGAAATGATGTGGGAGGTTACCTTTCTACAACCAAGGACCATGAGAACTTTTT	660
Db	1053	ATGTATGAAATGATGTGGGAGGTTACCTTTCTACAACCAAGGACCATGAGAACTTTTT	1112
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Qy	721	TTCCTTTTCAGGGCTCTTGATTAAGGATCCAAATAAACGCCTTGGTGGAGGACCAAGATGAT	780
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Db	1233	GCAAAAGAAATTATGAGACACAGTTTCTCTCTGAGTAAACTGGCAAGATGTATATGAT	1292
Qy	841	AAAAAGCTTGTACCTCTCTTTTAAACCTCAAGTAACATCTGAGACAGATACCTAGATATTTT	900
Db	1293	AAAAAGCTTGTACCTCTCTTTTAAACCTCAAGTAACATCTGAGACAGATACCTAGATATTTT	1352
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Db	1353	GATGAAGAAATTACAGCTCAGACTATTACAATAACACCACTGAAATAATATGATGAGAT	1412
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Db	1413	GGTATGGACTCATGGAC	1430

RESULT 14  
AF124141  
LOCUS AF124141 1708 bp mRNA linear PRI 07-MAY-1999  
DEFINITION Homo sapiens protein kinase B gamma mRNA, complete cds.  
ACCESSION AF124141

AF124141.1	GI:4757578	
VERSION	Homo sapiens (human)	
KEYWORDS	Homo sapiens	
SOURCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.	
ORGANISM	1 (bases 1 to 1708)	
REFERENCE	Brodbeck,D., Cron,P. and Hemmings,B.A.	
AUTHORS	A human protein kinase Bgamma with regulatory phosphorylation sites in the activation loop and in the C-terminal hydrophobic domain	
TITLE	J. Biol. Chem. 274 (14), 9133-9136 (1999)	
JOURNAL	10092583	
PUBMED	2 (bases 1 to 1708)	
REFERENCE	Brodbeck,D., Cron,P. and Hemmings,B.A.	
AUTHORS	Direct Submission	
TITLE	Submitted (27-JAN-1999) Friedrich Miescher-Institut, Maulbeerstrasse 66, Basel 4058, Switzerland	
JOURNAL	Location/Qualifiers	
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ORIGIN		
Query Match	100.0%;	Score 978; DB 8; Length 1708;
Best Local Similarity	100.0%;	Pred. No. 4e-206;
Matches 978; Conservative	0; Mismatches	0; Indels 0; Gaps 0;
Qy	1	TCTACAAACCCATATAAAGAAAGACAAATGAATGATTTTGGACTATTTTGAAACTACTAGGT 60
Db	418	TCTACAAACCCATATAAAGAAAGACAAATGAATGATTTTGGACTATTTTGAAACTACTAGGT 477
Qy	61	AAAGGCACCTTTTGGGAAAGTTATTTTGGTTCGAGAGAAGGCAAGTGGAAATATCTATGCT 120
Db	478	AAAGGCACCTTTTGGGAAAGTTATTTTGGTTCGAGAGAAGGCAAGTGGAAATATCTATGCT 537
Qy	121	ATGAGAGATTTGAGAAAGAGTCAATTATTGTCAAAGGATGAAGTGGCACACACTCTAACT 180
Db	538	ATGAGAGATTTGAGAAAGAGTCAATTATTGTCAAAGGATGAAGTGGCACACACTCTAACT 597
Qy	181	GAAGAGCAGAGTATTAAAGAACACACTAGACATCCCTTTTAAACATCCTTGAATATTTCCCTTC 240
Db	598	GAAGAGCAGAGTATTAAAGAACACACTAGACATCCCTTTTAAACATCCTTGAATATTTCCCTTC 657
Qy	241	CAGACAAAAGACCGTTTGTGTTTGTGATGGAATATGTTAATGGGGCGAGCTGTTTTTC 300
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Qy	361	GTCTCTGCTTGGACTATCTACATTCGGGAAAGATTGTGTACCGTGATCTCAAGTTGGAG 420
Db	778	GTCTCTGCTTGGACTATCTACATTCGGGAAAGATTGTGTACCGTGATCTCAAGTTGGAG 837
Qy	421	AATCTAATGCTGGCAAAAGATGGCCACATAAAATTACAGATTTTTGGACTTTGCAAGAA 480



Result No.	Score	Query		Length	DB	ID	Description
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2	978	100.0	100.0	1436	6	A0206530	Sequence
3	978	100.0	100.0	1440	6	B0142211	Method fo
4	978	100.0	100.0	1440	11	AY335691	Synthetic
5	978	100.0	100.0	1440	11	AY893474	Synthetic
6	978	100.0	100.0	1440	11	AY893919	Synthetic

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PC C12N5/00,A61K37/60
CC Human Akt-3
FH Key
FT source 1. .1435 Location/Qualifiers
FT /organism='Homo sapiens (human)'.
FEATURES
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ORIGIN
Query Match 100.0%; Score 978; DB 6; Length 1436;
Best Local Similarity 100.0%; Pred. No. 4.1e-206;
Matches 978; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TCTACAACCCATCATAAAGAAGCAATGAATGATTTTGGACTATTTGAAACTACTAGGT 60
DB 406 TCTACAACCCATCATAAAGAAGCAATGAATGATTTTGGACTATTTGAAACTACTAGGT 465
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DB 586 GAAAGCAGAGTATTAAGAACAACACTAGACATCCCTTTTAAACATCTTGAATATTTCCCTTC 645
QY 241 CAGACAAAAGACCGTTTGTGTTTGTGATGGAATATGTTAATGGGGGGGAGCTGTTTTC 300
DB 646 CAGACAAAAGACCGTTTGTGTTTGTGATGGAATATGTTAATGGGGGGGAGCTGTTTTC 705
QY 301 CATTTGTCGAGAGAGCGGTGTTTCTGAGGACCGGACACACGTTTCTATGGTGCAGAAAT 360
DB 706 CATTTGTCGAGAGAGCGGTGTTTCTGAGGACCGGACACACGTTTCTATGGTGCAGAAAT 765
QY 361 GTCTGCTGCTGGACTATCTACATTCGGAAGAGTTGTACCGTGATCTCAAGTTGGAG 420
DB 766 GTCTGCTGCTGGACTATCTACATTCGGAAGAGTTGTACCGTGATCTCAAGTTGGAG 825
QY 421 AATCTAATGCTCGACAAAGATGGCCACATAAAATTTACAGATTTTGGACTTTGCAAGAA 480
DB 826 AATCTAATGCTCGACAAAGATGGCCACATAAAATTTACAGATTTTGGACTTTGCAAGAA 885
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DB 886 GGGATCAGAGATGCAGCCACCATTGAAGACATTTCTGTGGCACTCCAGAAATPACTGGACCA 945
QY 541 GAGGTGTTAGAGATAATGACTATGCGCCGACGAGTAGCTGTTGGGGCTAGGGGTTGTC 600
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QY 841 AAAAGCTTGTACCTCCTTTTAAACCTCAAGTAACATCTGAGACAGATAGATATTTT 900
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DB 1366 GGTATGGACTGCATGGAC 1383

RESULT 2
AX026530 1436 bp DNA linear PAT 16-SEP-2000
DEFINITION Sequence 2 from Patent WO0037613.
ACCESSION AX026530
VERSION AX026530.1 GI:10187718
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Masure,S.L. and Richardson,A.
TITLE Human akt-3
JOURNAL Patent: WO 0037613-A 2 29-JUN-2000;
MASURE STEFAN LEO JOZEF (BE) ; RICHARDSON ALAN (BE) ; JANSSEN
PHARMACEUTICA NV (BE)
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Query Match 100.0%; Score 978; DB 6; Length 1436;
Best Local Similarity 100.0%; Pred. No. 4.1e-206;
Matches 978; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TCTACAACCCATCATAAAGAAGCAATGAATGATTTTGGACTATTTGAAACTACTAGGT 60
DB 406 TCTACAACCCATCATAAAGAAGCAATGAATGATTTTGGACTATTTGAAACTACTAGGT 465
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RESULT 3
BD142211 LOCUS BD142211 1440 bp DNA linear PAT 18-SEP-2002
DEFINITION Method for controlling apoptosis and polypeptide controlling
apoptosis.
ACCESSION BD142211
VERSION BD142211.1 GI:23237156
KEYWORDS WO 0215925-A/5.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 1440)
Tsuruo, T., Fujita, N. and Sato, S.
Method for controlling apoptosis and polypeptide controlling
TITLE Patent: WO 0215925-A 5 28-FEB-2002;
JOURNAL KYOWA HAKKO KOGYO CO LTD, TAKASHI TSURUO, NAOYA FUJITA, SAORI SATO
COMMENT OS Homo sapiens (human)
PN WO 0215925-A/5
PD 28-FEB-2002
PF 22-AUG-2001 WO 2001JP007179
PR 22-AUG-2000 JP 00P 251529
PI TAKASHI TSURUO, NAOYA FUJITA, SAORI SATO
PC A61K38/17, A61K38/45, A61K39/395, A61K45/00, A61P43/00, A61P3/08,
PC A61P35/00,
PC A61P43/00, C07K7/04, C07K14/47, C07K16/18, C12N1/15, C12N1/19 PC
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Matches 978; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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LOCUS AY893474 1440 bp mRNA linear SYN 16-MAR-2005  
DEFINITION Synthetic construct Homo sapiens clone FLH127839.01X v-akt murine  
thymoma viral oncogene-like 3 (AKT3) mRNA, complete cds.  
ACCESSION AY893474  
VERSION 1 GI:60819745  
KEYWORDS Human ORF Project.  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.  
REFERENCE 1 (bases 1 to 1440)  
AUTHORS Hines, L., Taron, B., Jepson, D., Moreira, D., Raphael, J., Shen, B.,  
Halleck, A., Koundinya, M., Hu, Y., Zuo, D. and Labaer, J.  
TITLE Cloning of human full-length CDS FLXGene in  
Gateway(TM) recombinational vector system  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 1440)  
AUTHORS Hines, L., Taron, B., Jepson, D., Moreira, D., Raphael, J., Shen, B.,  
Halleck, A., Koundinya, M., Hu, Y., Zuo, D. and Labaer, J.  
TITLE Direct Submission  
JOURNAL Submitted (04-JAN-2005) Biological Chemistry and Molecular  
Pharmacology, Harvard Institute of Proteomics, 320 Charles St.,  
Cambridge, MA 02141, USA  
COMMENT This CDS clone is a part of a collection of human full-length  
expression clones generated by Harvard Institute of Proteomics.  
This ORF clone has been cloned with normalized stop-codon. AttB  
recombination sites have been added to either end of the ORF and  
directionally cloned using the Gateway cloning system into pDONR  
201. Additional sequences in the clone: 'ACC' before the 'ATG'  
(corresponding to ribosomal binding site and Kozak consensus  
sequences). Each clone is clonally isolated and full-length  
sequence-verified.  
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from placenta and brain"  
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ORIGIN  
Query Match 100.0%; Score 978; DB 11; Length 1440;  
Best Local Similarity 100.0%; Pred. No. 4.1e-206;  
Matches 978; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 TCTACAACCCATCATATAAGAAAGACAAATGAATGATTTTGACTATTGAACTACTAGGT 60  
Db 406 TCTACAACCCATCATATAAGAAAGACAAATGAATGATTTTGACTATTGAACTACTAGGT 465  
Qy 61 AAAGGCATTTTGGGAAGTATTATTTGGTTCGAGAGAGGCAAGTGGAAATATATGCT 120  
Db 466 AAAGGCATTTTGGGAAGTATTATTTGGTTCGAGAGAGGCAAGTGGAAATATATGCT 525

Qy 121 ATGAAGATTCTTGAGAAAGAAAGTCAATATTGCAAAAGATGAAGTGGCACACACTCTAACT 180  
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Qy 241 CAGACAAAAGACCGTTTGTGTTTGTGATGGAATATGTTAATGGGGCGAGCTGTTTTTC 300  
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Qy 301 CATTTGTGAGAGAGCGGGTGTCTCTGAGGACCGCACACAGTTTCTATGTTGCGAGAAATT 360  
Db 706 CATTTGTGAGAGAGCGGGTGTCTCTGAGGACCGCACACAGTTTCTATGTTGCGAGAAATT 765  
Qy 361 GTCTCTGCCCTTGACATCTACATTCGGGAAAGATTGTGTACCGTGATCTCAAGTTGGAG 420  
Db 766 GTCTCTGCCCTTGACATCTACATTCGGGAAAGATTGTGTACCGTGATCTCAAGTTGGAG 825  
Qy 421 AATCTAATGCTGGACAAAGATGGCCACATATAAATAATACAGATTTTGGACITTTGCAAGAA 480  
Db 826 AATCTAATGCTGGACAAAGATGGCCACATATAAATAATACAGATTTTGGACITTTGCAAGAA 885  
Qy 481 GGGATCACAGATGCAGCCACCATGAAGACATTTCTGTGGCACTCCAGAAATATCTGGCACCA 540  
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Qy 961 GGTATGACCTGCATGGAC 978  
Db 1366 GGTATGACCTGCATGGAC 1383  
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AY893919 1440 bp mRNA linear SYN 16-MAR-2005  
LOCUS Synthetic construct Homo sapiens clone FLH127915.01L v-akt murine  
DEFINITION thymoma viral oncogene-like 3 (AKT3) mRNA, partial cds.  
ACCESSION AY893919  
VERSION 1 GI:60831074  
KEYWORDS Human ORF Project.  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.  
REFERENCE 1 (bases 1 to 1440)



AUTHORS	Hines, L., Taron, B., Jenson, D., Moreira, D., Raphael, J., Shen, B., Halleck, A., Koundinya, M., Hu, Y., Zuo, D. and Labaer, J.
TITLE	Cloning of human full-length CDS FLEXGene in Gateway(TM) recombination vector system
JOURNAL	Unpublished
REFERENCE	2 (bases 1 to 1440)
AUTHORS	Hines, L., Taron, B., Jenson, D., Moreira, D., Raphael, J., Shen, B., Halleck, A., Koundinya, M., Hu, Y., Zuo, D. and Labaer, J.
TITLE	Direct Submission
JOURNAL	Submitted (04-JAN-2005) Biological Chemistry and Molecular Pharmacology, Harvard Institute of Proteomics, 320 Charles St., Cambridge, MA 02141, USA
COMMENT	This CDS clone is a part of a collection of human full-length expression clones generated by Harvard Institute of Proteomics. This ORF clone has been cloned without stop-codon (to allow fusion with C-terminal tag). AtB recombination sites have been added to either end of the ORF and directionally cloned using the Gateway cloning system into pDONR 201. Additional sequences in the clone: 'ACC' before the 'ATG' (corresponding to ribosomal binding site and Kozak consensus sequence). Each clone is clonally isolated and full-length sequence-verified.
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ORIGIN	
Query Match	100.0%; Score 978; DB 11; Length 1440;
Best Local Similarity	100.0%; Pred. No. 4.1e-206;
Matches 978; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
QY	1 TCTACAACCCATCAATAAAGAAAGACAATGAATGATTTTGACATATTGTAAGAACTACTAGT 60
DB	
QY	406 TCTACAACCCATCAATAAAGAAAGACAATGAATGATTTTGACATATTGTAAGAACTACTAGT 465
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QY	61 AAAGGCACATTTGGGAAGCTATTTTGGTTCGAGAGAGCAAGTGGAAATACTATGCT 120
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DB	
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DB	
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DB	
QY	181 GAAAGCAGAGTATTAAGAACAACACTAGACATCCCTTTTAAACATCCCTTGAATATTCCCTTC 240
DB	
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DB	
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DB	

Db	646 CAGACAAAAGACCGTTTGTGTTTGTGATGGAATATGTTAATGGGGCGAGCTGTTTTC 705
QY	301 CATTTGTGCGAGAGACGGGTGTTCTCTGAGGACCGCACACAGTTTCTATGTCAGAAAT 360
DB	
QY	706 CATTTGTGCGAGAGACGGGTGTTCTCTGAGGACCGCACACAGTTTCTATGTCAGAAAT 765
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QY	361 GTCCTGCTTGGACTATCTACATTTCCGGAAGATTGTACCGTGATCTCAAGTTGGAG 420
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QY	766 GTCTCTGCTTGGACTATCTACATTTCCGGAAGATTGTGTACCGTGATCTCAAGTTGGAG 825
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QY	421 AATCTAATGCTCGACAAAGATGCCACATAAAAAATTTACAGATTTTGGACTTTGCAAGAA 480
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QY	886 GGGATCACAGATGCGAGCCACCATGAAGACATTCTGTGGCACTCCAGAAATATCTGGCACCA 945
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QY	541 GAGGTGTTAGAGATAATGACTATGCGCGAGCAGTAGCTGTGGGGCCTAGGGGTGTC 600
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QY	1006 ATGTATGAATGATGTGGGAGGTTTACCTTTCTACAACCCAGACCATCAGAAACTTTT 1065
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QY	1066 GAATTAATTAATGAAGACACATTAATAATTTCTCGAACAACCTCTCTTCAGATGCAAAATCA 1125
DB	
QY	721 TTGCTTTGAGGCTCTTGATTAAGGATCCAAATAAACCGCTTGTGGAGGACCATGATGAT 780
DB	
QY	1126 TTGCTTTGAGGCTCTTGATTAAGGATCCAAATAAACCGCTTGTGGAGGACCATGATGAT 1185
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QY	781 GCAAAAGAAATTTATGAGACACAGTTTCTCTCTGAGTAAACTGGCAAGATGTATATGAT 840
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QY	841 AAAAAAGCTTGTACCTCTCTTTTAAAGCTCAAGTAAACATCTGAGACAGATAGATATTTT 900
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QY	1246 AAAAAAGCTTGTACCTCTCTTTTAAAGCTCAAGTAAACATCTGAGACAGATAGATATTTT 1305
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QY	901 GATGAAGAAATTTACAGCTCAGACTATTAATAAACAACACACCTGAAATAATATGATGAGAT 960
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QY	1306 GATGAAGAAATTTACAGCTCAGACTATTAATAAACAACACACCTGAAATAATATGATGAGAT 1365
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RESULT 7	
BC020479	
LOCUS	1445 bp mRNA linear PRI 28-JUL-2005
DEFINITION	Homo sapiens v-akt murine thymoma viral oncogene homolog 3 (protein kinase B, gamma), mRNA (cdna clone IMAGE:3867931), partial cds.
ACCESSION	BC020479
VERSION	BC020479.1 GI:18042842
KEYWORDS	
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.
AUTHORS	1 (bases 1 to 1445)
	Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.P., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Uscin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,

Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butlerfield, Y.S., Krzywinski, M.I., Skaleka, U., Smailus, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.  
Mammalian Gene Collection Program Team  
Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences  
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)  
12477932  
2 (bases 1 to 1445)  
NIH MGC Project  
Direct Submission  
Submitted (03-JAN-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Bethesda, MD 20892-2590, USA  
NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
Contact: MGC help desk  
Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
Tissue Procurement: ATCC  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)  
DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center  
Center code: BCM-HGSC  
Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>  
Contact: [amg@bcm.tmc.edu](mailto:amg@bcm.tmc.edu)  
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H., Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati, A.N., Gibbs, R.A.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILNL at: <http://image.llnl.gov>  
Series: IRAK Plate: 13 Row: h Column: 23  
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 32307164.  
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ORIGIN

Query Match	100.0%;	Score 978;	DB 8;	Length 1445;
Best Local Similarity	100.0%;	Pred. No. 4.1e-206;		
Matches 978;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	TCTACACCCATCATATAAAGACACAAATGAATGATTTTGACATATTTTGAAACTACTAGGT	60	
Db	452	TCTACACCCATCATATAAAGACACAAATGAATGATTTTGACATATTTTGAAACTACTAGGT	511	
Qy	61	AAAGGCACTTTTCGGAAGTTATTTTCGTCGAGAGAAGCAAGTCGGAATACTATGCT	120	
Db	512	AAAGGCACTTTTCGGAAGTTATTTTCGTCGAGAGAAGCAAGTCGGAATACTATGCT	571	
Qy	121	ATGAAGATTCTGAAGAAAGAGTCATTATTATGCAAAAGGATGAAGTGGCACACACTCTAACT	180	
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Qy	181	GAAGCAGAGTATTAAAGAACACATAGACATCCCTTTTAAACATCCTTGAATAATTCCTTC	240	
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Qy	241	CAGACAAAACACCGTTTGTGTTTGTGATGGAATATGTTAATGGGGCGAGCTGTTTTTC	300	
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 REFERENCE 1 (bases 1 to 1547)  
 AUTHORS Masure,S.L.J. and Richardson,A.  
 TITLE Human Akt-3  
 JOURNAL JANSSEN PHARMACEUTICA NV  
 COMMENT OS Homo sapiens (human)  
 PN JP 2002535964-A/1  
 PD 29-OCT-2002  
 PF 17-DEC-1999 JP 2000589669  
 PR 22-DEC-1998 GB 9828375.7  
 PI STEFAN LEO JOZEF MASURE,ALAN RICHARDSON  
 PC C12N15/09,A61K31/713,A61K38/53,A61K39/395,A61K48/00,PC A61P35/00,  
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 1 TCTACAACCCATATAAAGAACAAATGAATGATTTGACTATTTGAAACTACTAGGT 60  
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 181 GAAAGCAGAGTATTAAAGAACACATAGACATCCCTTTTAAACATCCTTTGAAATATCTCTTC 240  
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 241 CAGACAAAGACCGTTTGTGTTTGTGATGGAATATGTTAATGGGGGAGCTGTTTTTC 300  
 656 CAGACAAAGACCGTTTGTGTTTGTGATGGAATATGTTAATGGGGGAGCTGTTTTTC 715  
 301 CATTTGTCGAGAGAGCGGGTGTCTCTGAGGACCGCACACATGTTTCTATGGTGACAGAAAT 360  
 716 CATTTGTCGAGAGAGCGGGTGTCTCTGAGGACCGCACACATGTTTCTATGGTGACAGAAAT 775  
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Db 536 ATGAAGATTCTGAAGAAAGAGTCAATTATTCGAAGGATGAAGTGGCACACACTCTAACT 595  
Qy 181 GAAAGCAGAGTATTAAGAAACACATAGACATCCCTTTTAAACATCCTTGAATATTCCTTC 240  
Db 596 GAAAGCAGAGTATTAAGAAACACATAGACATCCCTTTTAAACATCCTTGAATATTCCTTC 655  
Qy 241 CAGACAAAGACCGTTTGTGTTTGTGATGAATATTAAGTGGGCGAGCTGTTTTTC 300  
Db 656 CAGACAAAGACCGTTTGTGTTTGTGATGAATATTAAGTGGGCGAGCTGTTTTTC 715  
Qy 301 CATTTGTCGAGAGCGGCTCTCTCGAGGACCGCACACGTTTCTATGTCGAGAAAT 360  
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Qy 361 GTCTCTGCTTTGGACTATCTACATTCGGAAGATTTGTGTACCGTGATCTCAAGTTGGAG 420  
Db 776 GTCTCTGCTTTGGACTATCTACATTCGGAAGATTTGTGTACCGTGATCTCAAGTTGGAG 835  
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Db 836 AATCTAATGCTGGACAAAGATGGCCACATATAAAATTCAGATTTTGAATTTGCAAGAA 895  
Qy 481 GGGATCACAGATGCAGCCACCATGAAGACATTCGTGSCATCTCAGAAATATCTGGCACCA 540  
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Qy 541 GAGGTGTTAGAGATAATGACTATGGCCGAGCAGTAGACTGGTGGGCGCTAGGGGTTGTC 600  
Db 956 GAGGTGTTAGAGATAATGACTATGGCCGAGCAGTAGACTGGTGGGCGCTAGGGGTTGTC 1015  
Qy 601 ATGATGAAATGATGTGGAGGTTTACCTTTCTACAAACCGACCATGAGAAACTTTTTT 660  
Db 1016 ATGATGAAATGATGTGGAGGTTTACCTTTCTACAAACCGACATGAGAAACTTTTTT 1075  
Qy 661 GAAATTAATTAATGGAAGACATTAATTTCTCGAACACATCTCTCAGATGCAAAATCA 720  
Db 1076 GAAATTAATTAATGGAAGACATTAATTTCTCGAACACATCTCTCAGATGCAAAATCA 1135  
Qy 721 TTGCTTTTCAGGCGCTTTGATGAGACAGATTTCTCTCGAGGTAAACTGGGAGGACAGATGAT 780  
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Qy 781 GCAAAAGAAATTTAGACACAGATTTCTCTCGAGGTAAACTGGGAGGACAGATGATGAT 840  
Db 1196 GCAAAAGAAATTTAGACACAGATTTCTCTCGAGGTAAACTGGGAGGACAGATGATGAT 1255  
Qy 841 AAAAGCTTTGACCTCTTTTAAACCTCAAGTAACTGAGACAGATGATGATGATGAT 900  
Db 1256 AAAAGCTTTGACCTCTTTTAAACCTCAAGTAACTGAGACAGATGATGATGATGAT 1315  
Qy 901 GATGAAGAAATTTACAGCTCAGACTATTAACAATAACACCCTGAAATATGATGAGGAT 960  
Db 1316 GATGAAGAAATTTACAGCTCAGACTATTAACAATAACACCCTGAAATATGATGAGGAT 1375  
Qy 961 GGTATGGAATGATGGAC 978  
Db 1376 GGTATGGAATGATGGAC 1393

RESULT 10  
AX026529 LOCUS AX026529 1547 bp DNA linear PAT 16-SEP-2000  
DEFINITION Sequence 1 from Patent WO0037613.  
ACCESSION AX026529  
VERSION AX026529.1 GI:10187717  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Homo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.  
1 Masure, S.L. and Richardson, A.  
AUTHORS Human akt-3  
TITLE Patent: WO 0037613-A 1 29-JUN-2000;  
JOURNAL MASURE STEFAN LEO JOZEF (BE) ; RICHARDSON ALAN (BE) ; JANSSEN PHARMACEUTICA NV (BE)  
FEATURES Location/Qualifiers  
source 1. 1547  
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ORIGIN  
Query Match 100.0%; Score 978; DB 6; Length 1547;  
Best local Similarity 100.0%; Pred. No. 4,1e-206;  
Matches 978; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 TCTACAAACCCATCATATAAAGAAAGACAAATGAATGATTTTGACTATTTTGAACACTACTAGGT 60  
Db 416 TCTACAAACCCATCATATAAAGAAAGACAAATGAATGATTTTGACTATTTTGAACACTACTAGGT 475  
Qy 61 AAAGGCACCTTTTGGGAAAGTTATTTTGGTTTCGAGAGAGGCAAGTGGAAATATCTATGCT 120  
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Db 536 ATGAAGATTTCTGAAGAAAGTCAATTTATTTGCAAGGATGAAGTGGGCACACACTCTAACT 595  
Qy 181 GAAAGCAGAGTATTAAGAAACACCTAGACATCCCTTTTAAACATCTCTTGAATATTTCTCTTC 240  
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Qy 241 CAGACAAAGACCGTTTGTGTTTGTGTGATGGAATATGTTAATGGGGCGAGCTGTTTTTC 300  
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Qy 301 CATTTGTCGAGAGCGGGTGTCTCTGAGGACCGCACACGTTTCTATGTCGAGAAAT 360  
Db 716 CATTTGTCGAGAGCGGGTGTCTCTGAGGACCGCACACGTTTCTATGTCGAGAAAT 775  
Qy 361 GTCTCTGCTTTGACTATCTACATTCGGAAGATTTGTGTACCGTGATCTCAAGTTGGAG 420  
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Qy 481 GGGATCACAGATGCAGCCACCATGAAGACATTCGTGSCATCTCAGAAATATCTGGCACCA 540  
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Qy 541 GAGGTGTTAGAGATAATGACTATGGCCGAGCAGTAGACTGGTGGGCGCTAGGGGTTGTC 600  
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Qy 661 GAAATTAATTAATGGAAGACATTAATTTCTCGAACACATCTCTCAGATGCAAAATCA 720  
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Db 1136 TTGCTTTTCAGGCGCTTTGATGAGAGGATCCAAATTAACGCGCTTGGTGGAGGACCAAGATGAT 1195  
Qy 781 GCAAAAGAAATTTAGACACAGATTTTCTCTCGAGGTAAACTGGGAGGACAGATGATGAT 840

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Db	1256	AAAAAGCTTGACCTCCTCTTTTAAACCTCAAGTAACATCTGAGACAGATACAGATATTTT	1315	
Qy	901	GATGAAGAAATTTACAGCTCAGACTATTTACAAATTAACACCACCTGAAAAATATGATGAGGAT	960	
Db	1316	GATGAAGAAATTTACAGCTCAGACTATTTACAAATTAACACCACCTGAAAAATATGATGAGGAT	1375	
Qy	961	GGTATGACTGCATGGAC	978	
Db	1376	GGTATGACTGCATGGAC	1393	

RESULT 11

HSA245709

LOCUS Homo sapiens mRNA for serine/threonine kinase Akt-3 (Akt3 gene). 1547 bp mRNA linear PRI 15-APR-2005

DEFINITION Homo sapiens mRNA for serine/threonine kinase Akt-3 (Akt3 gene).

ACCESSION AJ245709

VERSION AJ245709.1 GI:5804885

KEYWORDS Akt-3; Akt3 gene.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

AUTHORS Masure, S., Haefner, B., Wesselink, J.J., Hoefnagel, E., Mortier, E., Verhasselt, P., Tuytelaars, A., Gordon, R. and Richardson, A.

TITLE Molecular cloning, expression and characterization of the human serine/threonine kinase Akt-3

JOURNAL Eur. J. Biochem. 265 (1), 353-360 (1999)

PUBMED 10491192

REFERENCE 2 (bases 1 to 1547)

AUTHORS Masure, S.L.

TITLE Direct Submission

JOURNAL Submitted (25-AUG-1999) Masure S.L., Biotechnology & High-Throughput Screening, Janssen Research Foundation, Turnhoutseweg 30, B-2340 Beerse, BELGIUM

COMMENT Phosphorylation at Thr305 and at Ser472 necessary for activation.

FEATURES

source

1. .1547

Location/Qualifiers

organism="Homo sapiens"

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/chromosome="1"

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/tissue\_type="human brain"

1. .>1547

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11. .1450

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/codon\_start=1

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Qy 901 GATGAAGAATTTACAGCTCAGACTATTACAATAACACACCTGAAATAATGATGAGGAT 960  
Db 1316 GATGAAGAATTTACAGCTCAGACTATTACAATAACACACCTGAAATAATGATGAGGAT 1375  
Qy 961 GGTATGAGCTCATGGAC 978  
Db 1376 GGTATGGACTCATGGAC 1393  
RESULT 12  
CQ714620  
LOCUS CQ714620 1651 bp DNA linear PAT 03-FEB-2004  
DEFINITION Sequence 554 from Patent WO02068579.  
ACCESSION CQ714620  
VERSION CQ714620.1 GI:42275477  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
REFERENCE 1  
AUTHORS Venter,C.J., Adams,M.C., Li,P.W. and Myers,E.W.  
TITLE Kits, such as nucleic acid arrays, comprising a majority of  
humanexons or transcripts, for detecting expression and other uses  
thereof  
JOURNAL Patent: WO 02068579-A 554 06-SEP-2002;  
PE Corporation (NY) (US)  
FEATURES  
source Location/Qualifiers  
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ORIGIN  
Query Match 100.0%; Score 978; DB 6; Length 1651;  
Best Local Similarity 100.0%; Pred. No. 4e-206;  
Matches 978; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 TCTACACCCATCATAAAGAAAGACAAATGAATGATTGTGACTATTGAAACTACTAGGT 60  
Db 361 TCTACACCCATCATAAAGAAAGACAAATGAATGATTGTGACTATTGAAACTACTAGGT 420  
Qy 61 AAAGCAGCTTTGGAAAGTTATTGTTGTCGAGAGAGGCAAGTGGAAATACATGCT 120  
Db 421 AAAGCAGCTTTGGAAAGTTATTGTTGTCGAGAGAGGCAAGTGGAAATACATGCT 480  
Qy 121 ATGAAGATTCTGAAGAAAGAGTCATTATTGCAAGAGGATGAAGTGGCACACACTCTAACT 180  
Db 481 ATGAAGATTCTGAAGAAAGAGTCATTATTGCAAGAGGATGAAGTGGCACACACTCTAACT 540  
Qy 181 GAAAGCAGAGTATTAAAGAACACTAGACATCCCTTTTAAACATCCCTTGAATAATTCCTTC 240  
Db 541 GAAAGCAGAGTATTAAAGAACACTAGACATCCCTTTTAAACATCCCTTGAATAATTCCTTC 600  
Qy 241 CAGACAAAGACCGTTGCTGTTTGTGATGCAATATGTTATGGGGCGAGCTGTTTTC 300  
Db 601 CAGACAAAGACCGTTGCTGTTTGTGATGCAATATGTTATGGGGCGAGCTGTTTTC 660  
Qy 301 CATTGTGTCGAGAGCGGGTGTCTCTGAGGACCGCACACAGTCTATGTCGACAGAAATT 360  
Db 661 CATTGTGTCGAGAGCGGGTGTCTCTGAGGACCGCACACAGTCTATGTCGACAGAAATT 720  
Qy 361 GTCTCTGCTTGGACTACTCTACATTCGGAAGAGTTGTTACCGTGATCTCAAGTTGGAG 420  
Db 721 GTCTCTGCTTGGACTACTCTACATTCGGAAGAGTTGTTACCGTGATCTCAAGTTGGAG 780  
Qy 421 AATCTAATGCTGGACAAAGATGGCCACATAAAATTACAGATTTTGGACTTTGCAAGAA 480  
Db 781 AATCTAATGCTGGACAAAGATGGCCACATAAAATTACAGATTTTGGACTTTGCAAGAA 840  
Qy 481 GGGATCACAGATGCAGGCCACCATGAAGACATTCTGTGGCACTCCAGAAATATCTGGCACCA 540

Db 841 GGGATCACAGATGCAGGCCACCATGAAGACATTCTGTGGCACTCCAGAAATATCTGGCACCA 900  
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Qy 601 ATGTATGAAATGATGTGTGGAGGTTACCTTTTCTACAACCAAGGACCATGAGAAACTTTTT 660  
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Qy 961 GGTATGAGCTGCATGGAC 978  
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RESULT 13  
AF085234  
LOCUS AF085234 1706 bp mRNA linear PRI 12-DEC-2001  
DEFINITION Homo sapiens STK-2 mRNA, complete cds.  
ACCESSION AF085234  
VERSION AF085234.1 GI:17529662  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
REFERENCE 1 (bases 1 to 1706)  
AUTHORS Li,X., Yu,L., Huang,H., Zhang,M., Zhao,Y. and Zhao,S.  
TITLE Cloning of a novel human cDNA, STK-2, which encodes a rat  
serine-threonine protein kinase (STK) homolog  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 1706)  
AUTHORS Zhao,Y.  
TITLE Direct Submission  
JOURNAL Submitted (22-AUG-1998) Zhao Y., Institute of Genetics, Fudan  
University, Lab of Human Gene Research, No. 220, Handan Road,  
Shanghai, People's Republic of China, 200433  
FEATURES  
source Location/Qualifiers  
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ORIGIN

Query Match		100.0%;	Score 978;	DB 8;	Length 1706;
Best Local Similarity		100.0%;	Pred. No. 4e-206;		
Matches 978;		Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	TCTACAACCCATCAATAAAGAAAGACAATGAATGATTTTGGACTATTGAAACTACTAGGT	60		
DB	453	TCTACAACCCATCAATAAAGAAAGACAATGAATGATTTTGGACTATTGAAACTACTAGGT	512		
QY	61	AAAGGCACCTTTTGGAAAGTTATTTTGGTTTCGAGAGAAGCGCAAGTGGAAATACTATGCT	120		
DB	513	AAAGGCACCTTTTGGAAAGTTATTTTGGTTTCGAGAGAAGCGCAAGTGGAAATACTATGCT	572		
QY	121	ATGAAGATCTCAAGAAAGAAAGTCAATATTGCAAAAGGATGAAGTGGCACACACTCTAACT	180		
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DB	753	CATTTGTGAGAGAGCGGTGTTCTCTGAGGACCGCACACAGTTTCTATGGTCAGAAAT	812		
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DB	813	GTCTCTGCTTGGACTATCTACATTCGGAAGATTTGTACCGTGATCTCAAGTTGGAG	872		
QY	421	AATCTAATGCTGGACAAAGATGCCACATATAAATTTACAGATTTTGGACTTTGCAAGAA	480		
DB	873	AATCTAATGCTGGACAAAGATGCCACATATAAATTTACAGATTTTGGACTTTGCAAGAA	932		
QY	481	GGGATCACAGATGCAGCCACCATGAAGACATTTCTGTGGCACTCCAGAATATCTGGACCA	540		
DB	933	GGGATCACAGATGCAGCCACCATGAAGACATTTCTGTGGCACTCCAGAATATCTGGACCA	992		
QY	541	GAGGTGTTAGAAGATAATGACTATGCGCGAGCAGTAGACTGTGGGGCCTAGGGGTTGTC	600		
DB	993	GAGGTGTTAGAAGATAATGACTATGCGCGAGCAGTAGACTGTGGGGCCTAGGGGTTGTC	1052		
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DB	1053	ATGTATGAAATGATGTGGGAGGTTTACCTTTCTACACCGAGCACCATGAGAAACTTTTT	1112		
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DB	1293	AAAAAGCTTGTAACCTCTTTTAAACCTCAAGTAACATCTGAGACAGACTAGATATTTT	1352		
QY	901	GATGAAGAAATTTACGCTCAGACTATTACAAATAACCAACCTGAAATAATGATGAGGAT	960		

Db	1353	GATGAAGAATTTACAGCTCAGACTATTACAATAACACACCTGAAAAATATGATGAGGAT	1412
QY	961	GGTATGAGCTGCATGGAC	978
Db	1413	GGTATGAGCTGCATGGAC	1430

RESULT 14

LOCUS	AF124141
DEFINITION	Homo sapiens protein kinase B gamma mRNA, complete cds.
ACCESSION	AF124141
VERSION	AF124141.1
GI	4757578
KEYWORDS	
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.
REFERENCE	1 (bases 1 to 1708)
AUTHORS	Brodbeck, D., Cron, P. and Hemmings, B.A.
TITLE	A human protein kinase Bgamma with regulatory phosphorylation sites in the activation loop and in the C-terminal hydrophobic domain
JOURNAL	J. Biol. Chem. 274 (14), 9133-9136 (1999)
PUBMED	10092583
REFERENCE	2 (bases 1 to 1708)
AUTHORS	Brodbeck, D., Cron, P. and Hemmings, B.A.
TITLE	Direct Submission
JOURNAL	Submitted (27-JAN-1999) Friedrich Miescher-Institut, Maulbeerstrasse 66, Basel 4058, Switzerland
FEATURES	Location/Qualifiers
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ORIGIN

Query Match		100.0%;	Score 978;	DB 8;	Length 1708;
Best Local Similarity		100.0%;	Pred. No. 4e-206;		
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QY	121	ATGAAGATCTCAAGAAAGAAAGTCAATATTGCAAAAGGATGAAGTGGCACACACTCTAACT	180		
DB	538	ATGAAGATCTCAAGAAAGAAAGTCAATATTGCAAAAGGATGAAGTGGCACACACTCTAACT	597		
QY	181	GAAAGCAGAGTATTAAGAAACAACACTAGACATCCCTTTTAAACATCTTGAATATTCCTTC	240		
DB	598	GAAAGCAGAGTATTAAGAAACAACACTAGACATCCCTTTTAAACATCTTGAATATTCCTTC	657		
QY	241	CAGACAAAAGACCGTTTGTGTTTGTGATGGAATATGTAATGGGGGGCAGCTGTTTTTC	300		



Db	658	CAGACAAAAGACCGTTTGTGTTTGTGATGGAATATGTTAATGGGCGGAGCTGTTTTTC	717
Qy	301	CATTTGTGCGAGAGCGGGTGTCTCTGAGGACCGCACACGTTTCTATGTTGCGAGAAATT	360
Db	718	CATTTGTGCGAGAGCGGGTGTCTCTGAGGACCGCACACGTTTCTATGTTGCGAGAAATT	777
Qy	361	GTCTCTGCCCTTGGACTATCTACATTTCCGGAAGAATTGTGTACCGTGATCTCAAGTTGGAG	420
Db	778	GTCTCTGCCCTTGGACTATCTACATTTCCGGAAGAATTGTGTACCGTGATCTCAAGTTGGAG	837
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Qy	481	GGGATCACAGATGCAGCCACCATGAAGACATTTCTGTGGCACTCCAGAAATATCTGGCACCA	540
Db	898	GGGATCACAGATGCAGCCACCATGAAGACATTTCTGTGGCACTCCAGAAATATCTGGCACCA	957
Qy	541	GAGGTGTTAGAAAGATAATGACTATGGCCGAGCAGTAGACTGGTGGGCGCTAGGGGTTGTC	600
Db	958	GAGGTGTTAGAAAGATAATGACTATGGCCGAGCAGTAGACTGGTGGGCGCTAGGGGTTGTC	1017
Qy	601	ATGTATGAATGATGTGTGGAGGTTACCTTTCTACAAACGAGCAGTGAAGAACTTTTT	660
Db	1018	ATGTATGAATGATGTGTGGAGGTTACCTTTCTACAAACGAGCAGTGAAGAACTTTTT	1077
Qy	661	GAATTAATATTAATGGAAGACATTTAAATTTTCTCGAACACTCTCTTCAGATGCAAAATCA	720
Db	1078	GAATTAATATTAATGGAAGACATTTAAATTTTCTCGAACACTCTCTTCAGATGCAAAATCA	1137
Qy	721	TTGCTTTTCAGGGCTCTTGATAAAGGATCCAAATAAACGCCCTTGGTGGAGGACGAGATGAT	780
Db	1138	TTGCTTTTCAGGGCTCTTGATAAAGGATCCAAATAAACGCCCTTGGTGGAGGACGAGATGAT	1197
Qy	781	GCAAAAGAAATTAATGAGACACAGTTTCTCTCTGGAGTAAACTGGCAAGATGTATATGAT	840
Db	1198	GCAAAAGAAATTAATGAGACACAGTTTCTCTCTGGAGTAAACTGGCAAGATGTATATGAT	1257
Qy	841	AAAAAGCTTGTAACCTCTTTTAAACCTCAAGTAACTCTGAGACAGATAGTATATTTT	900
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	Human protein kinase B-gamma polypeptide and method of degrading		
	nonhuman protein kinase B-gamma.		
ACCESSION	BD260777		
VERSION	BD260777.1	GI:33070547	
KEYWORDS	JP 2002539823-A/1.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;		
	Hominidae; Homo.		
REFERENCE	1	(bases 1 to 2367)	
AUTHORS	Attersand, A.		
TITLE	Human protein kinase B-gamma polypeptide and method of degrading		
JOURNAL	nonhuman protein kinase B-gamma		
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COMMENT	BIOVITRUM AB		
	OS Homo sapiens (human)		
	PN JP 2002539823-A/1		

PD	26-NOV-2002		
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PC	C12N9/12,C12Q1/48,C12Q1/68,G01N33/15,G01N33/50,G01N33/53,PC		
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CC	putative active phosphorylation site		
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ORIGIN			
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Best Local Similarity	100.0%;	Pred. No. 3.7e-206;	
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Qy	61	AAAGGCACTTTTGGGAAAGTTATTTTGGTTCGAGAGAGGCAAGTGGAAATATCTATGCT	120
Db	475	AAAGGCACTTTTGGGAAAGTTATTTTGGTTCGAGAGAGGCAAGTGGAAATATCTATGCT	534
Qy	121	ATGAAGATTTCTGAAGAAAGAGTCATTTATTCGAAAGGATGAAGTGGCACACACTCTAACT	180
Db	535	ATGAAGATTTCTGAAGAAAGAGTCATTTATTCGAAAGGATGAAGTGGCACACACTCTAACT	594
Qy	181	GAAAGCAGAGTATTAAAGAACACCTAGACATCCCTTTTAAACATCCTTTGAAATATTCCTTC	240
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Qy	241	CAGACAAAAGACCGTTTGTGTTTGTGATGGAATATGTTAATGGGGCGAGCTGTTTTTC	300
Db	655	CAGACAAAAGACCGTTTGTGTTTGTGATGGAATATGTTAATGGGGCGAGCTGTTTTTC	714
Qy	301	CATTGTGCGAGAGCGGGTGTCTCTGAGGACCGCACACGTTTCTATGTTGCGAGAAATT	360
Db	715	CATTGTGCGAGAGCGGGTGTCTCTGAGGACCGCACACGTTTCTATGTTGCGAGAAATT	774
Qy	361	GTCTCTGCCCTTGGACTATCTACATTCGCGAAAGATTGTGTACCGTGATCTCAAGTTGGAG	420
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Qy	481	GGGATCACAGATGCAGCCACCATGAAGACATTTCTGTGGCACTCCAGAAATATCTGGCACCA	540
Db	895	GGGATCACAGATGCAGCCACCATGAAGACATTTCTGTGGCACTCCAGAAATATCTGGCACCA	954
Qy	541	GAGGTGTTAGAAAGATAATGACTATGGCGGAGCAGTAGACTGGTGGGCGCTAGGGGTTGTC	600
Db	955	GAGGTGTTAGAAAGATAATGACTATGGCGGAGCAGTAGACTGGTGGGCGCTAGGGGTTGTC	1014
Qy	601	ATGTATGAATGATGTGTGGAGGTTTACCTTTTCTACAAACGAGCAGTGAAGAACTTTTT	660
Db	1015	ATGTATGAATGATGTGTGGAGGTTTACCTTTTCTACAAACGAGCAGTGAAGAACTTTTT	1074
Qy	661	GAATTAATATTAATGGAAGACATTAATTTCTCCTCGAACACTCTCTTCAGATGCAAAATCA	720
Db	1075	GAATTAATATTAATGGAAGACATTAATTTCTCCTCGAACACTCTCTTCAGATGCAAAATCA	1134



Qy	721	TTGCTTTCAGGGCTCTTGATAAAGGATCCAAATTAACCGCTTGGTGGAGGACCAGATGAT	780
Db	1135	TTGCTTTCAGGGCTCTTGATAAAGGATCCAAATTAACCGCTTGGTGGAGGACCAGATGAT	1194
Qy	781	GCAAAAGAAATTATGAGACACACAGTTTCTTCTCTGGAGTAAACTGGCAAGATGTATATGAT	840
Db	1195	GCAAAAGAAATTATGAGACACACAGTTTCTTCTCTGGAGTAAACTGGCAAGATGTATATGAT	1254
Qy	841	AAAAAGCTTGTAACCTCCTTTTAAACCTCAAGTAAACATCTGAGACAGATACTAGATATTTT	900
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Qy	901	GATGAGAAATTACAGCTCAGACTATTACAATAACACACCCTGAAAAATATGATGAGGAT	960
Db	1315	GATGAGAAATTACAGCTCAGACTATTACAATAACACACCCTGAAAAATATGATGAGGAT	1374
Qy	961	GGTATGGACTGCATGGAC	978
Db	1375	GGTATGGACTGCATGGAC	1392

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